

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Sun Jun 29 19:59:11 1997; MasPar time 1159.38 Seconds 903.507 Million cell updates/sec

Description:
Perfect Score:
N.A. Sequence:
Comp: Title: >US-08-663-618A-1 (1-1636) from US08663618A.seq 1636

Scoring table: TABLE default Gap 6

Nmatch STD Dbase 0; Query 0

Searched: 886179 seqs, 320143548 bases ×

Post-processing: Minimum Match 0% Listing first 45 summaries

EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 15:EST19 10:EST10 11:EST11 13:EST13 14:EST14 15:EST29 10:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 12:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST22 23:EST23 24:EST34 25:EST35 26:EST36 33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44 45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST56 57:EST57 58:EST56 53:EST53 54:EST54 55:EST55 56:EST56 63:EST56 64:EST66 65:EST56 66:EST56 67:EST67 68:EST68 69:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST64 67:EST77 71:EST77 72:EST77 73:EST77 74:EST74 74:EST88 89:EST89 80:EST89 80:EST99 90:EST99 91:EST97 98:EST99 93:EST99 94:EST99 96:EST99 97:EST97 98:EST99

EST-STS-TWO 105:EST110 105:EST110 110:EST111 110:EST111 120:EST120 125:EST125 130:EST135 140:EST140 145:EST140 145:EST140 145:EST140 155:EST155 0101:EST101 106:EST1101 111:EST111 116:EST111 121:EST121 126:EST121 121:EST121 121:EST121 131:EST131 131:EST131 136:EST146 141:EST146 141:EST146 151:EST150 151:EST150 151:EST150 151:EST150 151:EST150 151:EST150 171:EST150 1 122:EST122 5 127:EST127 5 137:EST137 5 137:EST137 1 142:EST142 6 147:EST142 1 152:EST147 1 152:EST152 5 157:EST157 162:EST162 153:EST153 158:EST158 163:EST163 138:EST138 143:EST143 148:EST148 123:EST123 128:EST128 133:EST133 103:EST103 108:EST108 113:EST113 118:EST118 3 104.EST104 8 109.EST109 3 114.EST111 8 119.EST112 8 124.EST112 8 129.EST124 8 129.EST134 8 139.EST134 8 139.EST134 8 149.EST144 8 149.EST149 8 159.EST154 8 159.EST154 8 169.EST159 8 169.EST169 8 169.EST169

Database:

Database: EST-STS-THREE

194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6 200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12 206:gnEST1 207:gnEST2 208:gnEST3 209:gnEST4 210:gnEST5 211:gnEST5 207:gnEST2 208:gnEST3 209:gnEST9 215:gnEST10 216:gnEST11 217:gnEST12 218:gnEST3 219:gnEST1 224:enEST2 220:gnEST12 217:gnEST12 218:gnEST3 219:gnEST13 219:gnEST1 224:enEST2 225:enEST3 231:enEST4 227:enEST5 228:enEST5 229:enEST7 230:enEST3 235:enEST4 237:enEST5 238:enEST5 235:enEST5 235:enEST1 235:enEST1 235:enEST1 235:enEST1 236:enEST1 240:enEST1 240:enEST2 245:enEST2 346:enEST2 247:enEST2 248:enEST2 249:enEST2 250:enST2 175:EST175 176:EST176 180:EST180 181:EST181 185:EST185 186:EST186 190:EST190 191:EST191 177:EST177 178:EST176 179:EST179 180:EST182 183:EST183 184:EST184 187:EST187 188:EST188 189:EST189 192:EST192 193:EST193

Statistics: Mean 11.516; Variance 2.174; scale 5.296

Pred. No. is the number of results predicted by chance to Prescore greater than or equal to the score of the result being and is derived by analysis of the total score distribution being printed, to have

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Result No.

Score

Query Match Length

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Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
WashU-Merck EST Project
WashU-Morn University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=-21m.3 Rsite1=EcoRI Rsite2=xhoI Normal lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                386;
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Source: IMAGE Consortium, LINL
This clone is available royalty-free th
IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
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Eutheria; Primates; Catarrhini; Hominidae;
I (bases 1 to 428)
Hillier,L., Clark,N., Dubuque,T., Elliston,
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1 (bases 1 to 405)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,I Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Mar. Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone=119384 library=Stratagene lung (#937210)
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a ;
year old male. Cloned unidirectionally. Primer: 011go dr. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GARITCGGCACGAG-3'; 3' adaptor sequence:
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
Washington University So
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Contact: Richard M. Myers Stanford Human Genome Center (SHGC)
Contact: Richard M. Myers Stanford Human Genome Center (SHGC)
C Stanford University School of Medicine Department of Genetics,
C M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689
C Email: myers@shgc.stanford.edu primer A: AAAGCCTGGAPAAAGGAACC
C Primer B: GCTGCACCTGGAATTGACTC STS size: 150 PCR Profile: Initial
C incubation: 94 degrees C for 90 seconds Denaturation: 94 degrees C for 15 seconds Denaturation: 94 degrees C for 15 seconds PCR Cycles: 30 Thermal
C Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1
C Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1
C UM dNTPS: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 10
C ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3
C Prepared with primer pairs derived from T94579--Merck/UniEST.
FH Key
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05-OCT-1996 (Rel. 49, L
human STS SHGC-17364
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Eukaryota; Animalia; Metazoa; Chordata; Vertebrata;
Theria; Eutheria; Primates; Haplorhini; Catarrhini;
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Similarity 97.1%;
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          STS
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/organism="Homo:
/map="1"
91..240
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          241 bp
SHGC-17364
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Last updated, Version
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                                   TGGGCCCAGCCTCAAAGCTGGGACTGGAGGGGGCTTTAGCGACTCAATTCCAGGTGCAGCA
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Primer B: GC:
STS size: 150
PCR Profile:
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 241)
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STS sequence;
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                                                                                                                                                                                                                                                                                                                                                             dNTPs:
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PCR Cycles:
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Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tangara, M., Tan, F., Tangara, T., Tangara, T
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l Similarity 63.3%;
197; Conservative
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High quality sequence stops: 323
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
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l (bases 1 to 541)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Holman,M., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Wohldmann,P. and
                                                                                                                                                                                               2.8%; ch 4.8%; l Similarity 66.7%; 166; Conservative
                                                                                                                                                                                                                                                                                                                                                   High quality sequence stops: 441
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                             WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VY29c01.rl Homo sapiens cDNA clone 244128 5' similar to gb:M8 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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/clone="244128"
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CTACTTCACCAACTGGGCCCAGTACAGACAGGGGGAGGCTCGCTTCCTGCCCAAGGACTT 138
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CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);...
N75653
                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800

Fax: 314 286 1810

Email: estévatson.wustl.edu

High quality sequence stops: 441

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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larity 66.7%;
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                                                                                                                     Score 78; DB 207;
Pred. No. 8.69e-99;
0; Mismatches 82;
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                                                                      ctcttcacatcatcatagcccacccacttggttccccttgactncgtaggggacctgctg 429
                                                                                                               GCCCAGACCATGGCCCCGCCCAGTCCCTTCTGCTTCAGATAGCTGACCTTGGTTTTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Werck EST Project
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                         4.5%;
1 Similarity 70.1%;
131; Conservation
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1 (bases 1 to 533)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human clone-81581 library-Stratagene lung (#937210)
vector-pBluescript SK- host-SOLR cells (kananycin resistant)
primer-21mi3 Rsitel=EcoRI Rsite2-XhoI Normal lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GARITCGCACGAC, 3', 3', adaptor sequence:
5'-CTCGAGTTTTTTTTTTTTTTTTTTTT-3'.
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s27879 SECRETORY PROTEIN
T65854
                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for fu focation/Qualifiers 1..533
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Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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Pred. No. 5.24e-89;
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TITLE
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TGGATGAGGGGGTATCGGCCCTGGTTGCAGGAGAAGCCGGCAAAGTCATCTAAGTCCAGT 1078
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Primer B: TCTCCCAGAATTCTCATGTGG
STS size: 132
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G24226
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Tel: 617 252 1900
Fax: 617 252 1902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae;
Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                            Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerase: 0.0
Total Vol: 20 ul
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                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                           KC1: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                                          MgCl2: 1.5 mM
KCl: 50 mM
                                                                                             Conservative
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WI-14165.
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/map="461.5 cR from top
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Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                         Score 73; DB 200;
Pred. No. 5.24e-89;
0; Mismatches 55.
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                                                                                ctgggcaggtgtagtggtcttgcttgcttctccagggaggatctgcctacaaactggtttg 128
CTGGGCAGGTTTCATGGTCCTGCTGATGATCCCATGGGGGCTCTGCTGCAAAACTGGTCTG 78
                                                                                                                        156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
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yw72b09.rl Homo sapiens cDNA clone 257753 5' similar to gb:M80927
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
WashU-Merck EST Project
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Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Bento Soares and M. Fatima Bonaldo
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                                                                                                                                     h 4.3%;
Similarity 65.8%;
                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
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/clone="257753"
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No. 3.96e-85;
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son,A., Wohldmann,P. and
                                                                                                                       80; Indels
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acaccaactggtcccagtaccgggaaggcaatgggagctgcttcccagacgccctcgacc
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                                                         TCACCAACTGGGCCCAGTACAGACAGGGGGGAGGCTCGCTTCCTGCCCAAGGACTTGGACC
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l Similarity 69.2%;
l37; Conservat
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similar to (
W51302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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Cloned unidirectionally. Primer: Oligo dT. pCMV-S
                                                                                                                                                                                                                                                                                /clone_lib="Life Tech mouse brain"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                              /clone="304743"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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Life Tech mouse brain Mus
gb:X93035 M.musculus mRNA
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Pred. No. 3.96e-85;
0; Mismatches 60
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Primer: Oligo dT. pCMV-SPORT2
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                                                                                                                   134 agctgg-cgggcgcatggtatgggccctngacctggatnacttncagggctccttctgcg 192
                                                                                                                                                                                                                                                                                                     14 ggaccacagtccatagaatcctcggccagcaggtcccctatgccaccaagggcaaccagt 73
                                                                                                                                                                                                            gggtaggatacgacgaccaggaaagcgtcaaaagcaaggtgcagtacctgaaggacaggc 133
                                                                                           GACTGGGCGGGCCATGGTCTGGGCACTGGACTTAGATGACTTTGCCGGCTTCTCCTGCA 1112
                                                                                                                                                                                    GGGTGGGCTTTGATGATGTGGAGAGCTTCAAAACCAAGGTCAGCTATCTGAAGCAGAAGG 1052
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Rifkin, E., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
Washington University S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Similarity 68.3%;
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/clone="160921"
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Pred. No. 1.59e-75;
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                                                                                                                               CCAGCCTTTGCACCCACCTCATCTACGCCTTCGCTGGCATGACCAAC
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           w10705 306 bp mRNA EST 26-APR-1996 ma47g07.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5' similar gb:m80927 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                              114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 396)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R55530 396 bp mRNA EST 22-MAY-1995
yj79c12.r1 Homo sapiens cDNA clone 154966 5' similar to gb:M8(
CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
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The WashU-Merck EST Project
W10705
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larity 68.3%;
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/clone="154966"
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Pred. No. 1.28e-73;
0; Mismatches 53;
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EST.
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                        ma47g07.
                                                                          W10705
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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Fax: 314 286 1810
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Similarity 72.1%;
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                                          306 bp mRNA EST Soares mouse p3NMF19.5 Mus musculus gb:M80927 CARTILAGE GLYCOPROTEIN-39
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Pred. No. 3.39e-64;
0; Mismatches 38
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Best Local Similarity 72.1%;
Matches 98; Conservative
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This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 172.
Location/Qualifiers
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WashU-HHMI Mouse EST Project
washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/Clone="313884"
/Clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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Direct Submission
Submitted (21-JUN-1995) Rolf G. Boot, Department of B. AMC, E.C. Slater, Institute, University of Amsterdam, 15, 1105 AZ, Amsterdam, The Netherlands
                                                                                                                       Aerts,J.M.
Cloning of a cDNA encoding chitotriosidase, produced by macrophages
J. Biol. Chem. 270 (44), 26252-26256 (1995)
                                                                                                                                                                                                                                                                                                                                       HSU29615 1633 bp
Human chitotriosidase
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                                                                          Boot, R.G.
                                                                                                                                                                                          Boot, R.G., Renkema, G.H., Strijland, A., van
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Result No.

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Statistics:

Mean 11.639;

Variance 4.516;

scale 2.577

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.

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Hakala,B.E., White,C. and Recklies,A.D.
Human cartilage gp-39, a major secretory product chondrocytes and synovial cells, is a mammalian m chitinase protein family
J. Biol. Chem. 268 (34), 25803-25810 (1993)
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ALDRFLCTHIIYSEANISUDHIDTWEWNDVTLYGGLAMLYPGRRDKQHFTTLIKEMKAE
FIKEAQPGKKOLLLSAALSAGKVTIDSSYDLAKISQHLDFISTMYYDFHGAWRGTTGH
HSPLFRGQEDASPDRFSNTDYAVGYMLRLGAAPSKLVMGIPTFGRSFTLASSETGVGA
PISGFOIFGRFYKEAGTLAYYEICDFLAGATVHRTLGQQVPYATKGNQMVGYDDQESV
KSKVOYLKDRQLAGAMVWALDLDDFQGSFCGQDLRFPLTNAIKDALAAT"
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/cell_type="chondrocyte"
/tissue_type="cartilage"
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(bases 1 to 1418)

Hu, B., Trinh, K., Figueira, W.F. and Price, P.A.

Isolation and sequence of a novel human chondrocyte protein related to mammalian members of the chitinase protein family

J. Biol. Chem. 271 (32), 19415-19420 (1996)
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Submitted (23-FEB-1996) Paul A. Price, Biology, 0322, California at San Diego, 9500 Gilman Drive, La Jolla, 92093-0322, USA
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FOKDFTKSTKERLLITAGVSAGROMIDNSYQVEKLAKDLDFINLLSFDFHGSWEKPLI
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99..1190
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1434)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Submitted (17-MAY-1996) Medical Biophysics, Institute, Princess Margaret Hospital, 610 Toronto, Ontario M5G 2M9, Canada
                                                                                                              Cloning of a novel lymphoid localization to 1p13.3
                                                       Grossman, A., and Mak, T.W.
                                                                                                                                                        Grossman, A., Matsuyama, T.,
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The WashU-Merck EST Project
                                         Direct Submission
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                                                                                                                                            and Mak, T.W.
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SAETTVGAPASGPGAAGPITESSGFLAYYEICQFLKGAKITRLQDQQVPYAVKGNQWV
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/gene="HUMTCHIT"
/note="32 A nucleotides"
/note="32 A nucleotides"
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37..114
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37..1209
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Institute, Princess Margaret Hospital, 610 U
Toronto, Ontario M5G 2M9, Canada
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Cloning of a novel lymphoid localization to 1p13.3
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                                                                    /product="chitinase"
//db_xref="pid:g1439568"
//db_xref="pid:g1439568"
//ta_xref="pid:g1439568"
//ta_xref="pid:g1439568"
//tagvvvllllogGsArklvcvftnwsQdrQsegkfftenideflcshliysfasien
kvilkdkseymlyQTinslkTknpklkillsiggylegSkgephpwdsStsklefin
SILHIRUNGSEDVSHIYPDQKENHHFTVLHELABAFQKDETKSTREFLLITAGV
SILHIRUNGSLDVSHIYPDQKENHFTVLHELABAFQKDFTKSTREFLLITAGV
SAGRQMIDNSYQVEKLAKDLDFINLSEDFHGSWEKPLITGHASPLSKGWQDDAGPSSY
YNVEYAVGYWIHKGMPSEKVVMGIPTYGHSFTLASAETTVGAFASGPGAAGPITESSG
FLAYYEICQFLKGAKITRLQDQQYPYAVKGNQWVGYDDVKSMETKVQFLKNLNLGGAM
                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/gene="HUMTCHIT"
/note="submitter can find no appropriate Kozak initiator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"Stratgene Jurkat T-cell cDNA library in Lambda Zap II; Clontech thymus polyA+ RNA; Stratagene placental genomic library in Lambda FIX II; activated T-cell plasmid library (Dr. Brian Seed)"
                                                                                                                                                                                                                                                                                                                           spliced form; see GenBank Ac
first alternatively spliced
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/map="1p13.3"
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143..172
  /gene="HUMTCHIT"
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                                                                              Direct Submission

Direct Submission

Submitted (19-JAN-1995) Millis A. J., University at Albany,

Biological Sciences, 1400 Washington Avenue, Albany, NY, USA, 12222

(bases 1 to 1733)

Shackelton, L. M., Mann, D. M. and Millis, A. J.

Identification of a 38-kba heparin-binding glycoprotein (gp38k) in

differentiating vascular smooth muscle cells as a member of a group

of proteins associated with tissue remodeling

J. Biol. Chem. 270 (22), 13076-13083 (1995)
                                                                                                                                                                                                                                                                                                           SSGP38KD 1733 bp RNA
S.scrofa 38kDa heparin-binding
Z47803
                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Su [ bases 1 to 1733)
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Sus scrofa
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/organism="Sus scrofa"
/clone="pBS38k"
/dev_stage="adult"
/tissue_type="smooth muscle"
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Sus scrofa
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Vertebrata;
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Identification of a 38-kDa heparin-binding glycoprotein (gp38k) differentiating vascular smooth muscle cells as a member of a gr of proteins associated with tissue remodeling J. Biol. Chem. 270 (22), 13076-13083 (1995)
                                                                                                                                                                                                                                                                                                                                                          Submitted (17-JAN-1995) Albert J.T. Millis, University at Albany, 1400 Washington Avenue Location/Qualifiers
                                         . Similarity 688; Conser
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Direct Submission
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larity 62.5%;
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a 507 c 463 g 355 t
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/dev_stage="adult"
67..1218
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RESULT 8

RESULT 8

AC 257803;

AC 277803;

NI 9634097

DI 19-JAN-199

DI 28-AUG-199

DE S.SCICGA 3

KW 9938k; hep

OC Theria; Eu

RN [2]

OC Theria; Eu

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RP 1-1733

RA Millis A.J

RI Submitted

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19-JAN-1995 (Rel. 42, Created)
28-AUG-1996 (Rel. 42, Last updated, Version S.scrofa 38kDa heparin-binding glycoprotein. 9p38k; heparin-binding glycoprotein. Sus scrofa (domestic pig)
Eukaryota; Animalia; Metazoa; Chordata; Vert
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"Identification of a 38-kDa heparin-binding glycoprotein in differentiating vascular smooth muscle cells as a memb group of proteins associated with tissue remodeling"; J. Biol. Chem. 270:13076-13083(1995).

Key

Location/Qualifiers
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J., University at Albany, Biological Sciences,
n Avenue, Albany, NY, USA, 12222
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larity 62.5%;
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/clone="pB538k"
/dev_stage-"adult"
/tissue_type-"smooth mus
/clone_lib-"lambda ZAP I
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RESULT S LOCUS DEFINITION ACCESSION

M.musculus X93035 MMBRP39

mRNA

1616 bp RNA for E

p RNA BRP39 p

protein

ROD

KEYWORDS SOURCE ORGANISM

g1085065 brp39 gene; house mouse.

BRP39

protein

Mus musculus Eukaryotae; mitochondrial Vertebrata; Eutheria; Rode

rial eukaryotes; Metazoa; Rodentia; Sciurognathi;

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/codon_start=1
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/translation="Mckraaligefavlmllqscsayklvcyftswsqyregvgsflpd
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Gekreselasnterriafvrsvapflrsygfdgldlamlyprlrdkqyfstlikelna
Eftkevqpgreklllsaalsagkvaidfydjaldfirlmtydphgvwrqitg
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HHSPpleqgkytdffedaysnyvaygyxirlfaadaskllhgliptgksftjlssenyl6
HPISGEGLPGRFTKEAGTLAYYEICDFLKGAEVHRLSNEKVPFATKGNQWVGYEHKES
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                                                                                            CTGGATTTTGTCAACCTTATGGCCTACGACTTCCATGGCTCTTGGGAGAAGGTCACGGGA
                                                                                                                                                                                                                     AATGCCTTCCAGCAGGAAGCCCAGACCTCAGGGAAGGAACGCCTTCTTCTGAGTGCAGCG
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/db_xref="PID:g1545819"
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/cell_type-"bone marrow
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Pred. No. 5.92e-91;
0; Mismatches 451;
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-SEP-1996) to the DDBJ/EMBL/GenBank databases. Makoto Owhashi, The University of Tokushima, Faculty of Integrated Arts and Sciences; 1-1 Minami-Johsanjima, Tokushima, Tokushima 770, Japan (E-mail:ohashi@ias.tokushima-u.ac.jp, Tel:0886-56-7261, Fax:0886-56-7298)
                                                                                                                                                                                                                                                                                                                           Owhashi,M., Arita,H., Taoka,Y. and Hayai,N. Molecular cloning and characterization of T eosinophil chemotactic factor (ECF-L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor,
D87757
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                                                       /codon_start=1
/product="ECF-L precursor"
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EMRKAFFEESVEKNIPKLLTTSTGAGIIDYIKGSYKIPELSOSLDYIOYMYVDLHDPK
CGYTGENSPLYKSPYDIGKSADLNVDSIISYWKDHGAASEKLIYGFPAYGHTFILSDF
SKTGIGAPTISTGAPPGKYTDESGLLAYYEVCTFLNEGATEVNDAPQEVPYAYQGNEWY
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                                                                                                                                                                                                                               /organism="Mus musculus"
/cell_type="bone marrow co
/tissue_type="bone marrow"
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          ttgaaggctcagtggctcaaggacaacaatttaggaggtgccgtggtcttggcgccttggac 1089
                                                          gtaccctatgcctatcagggtaatgagttgggttatgacaatgtcaggagcttcaag
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Best Local Similarity 59.7%;
Matches 370; Conservative
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gacagtcagattgtggccaaggatgcccgggatgagagcatcttctacccagagttcaac 256
                                                              CCCAAGGACTTGGACCCCAGCCTTTGCACCCACCTCATCTACGCCTTCGCTGGCATGACC 187
                                                                                                Sus scrofa complete cd. U43490
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Euhi, W.C., Choi, I., Cleaver, B.D. and Simmen, F.A.
Molecular cloning and characterization of an estrogen-dependen molecular cloning and characterization of postpopular or constitution of the constitution 
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/db_xref="piD:gl155332"
/translation="MGKLLWVGLVLVLKHHNGAAHKLVCYFANWAFSRPGPASILPR
/translation="MGKLLWVGLVLVLKHHNGAAHKLVCYFANWAFSRPGPASILPR
/translation="MGKLLWVGLVLVLKHHNGAHKLVCYFANWAFSRPGPASILPR
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green-"GTSRFTTMLSTFINREKFIRSAIGLLRTHGFDGLDLFFLYPGLRGSPRRDRWHFLFLL
EELLLAFREAQLTMRFRLLLSAAVSADPHVIQXAYDVLLGRLLDFINVISYDLHGS
WEKVYGHNSPLFSLSDDPKSSAYTMVWRKLGAPPEKLLMGFPTYGRTERLKASKNE
LGAEAVGPASPGKYTKQAGFLAYYEVCSFVQRAKKWIDHQYVPYAYRGKEWVGYDDD
ISFSYKAFFIKKEHFGGAMVWTLDLDDVRGTFCGTGFPFLYYMLNDLLLKAEVSSTLS
PGGGLSTVNSSRTCPESLAVIKDLTTDLGILPLGGEAVATETHGRSDNMTVTPGGGL
VAPTROTLSFGKLTVAFEGKTESPGEKAMTPVGHPSVTPGDMSVPPVPIQTGDRITPP
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74..1591
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/tissue_type="oviduct"
/dev_stage="adult"
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/strain="Crossbred Yorkshire
/clone="alv4"
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/sex="female"
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Submitted (28-OCT-1994) Mary M. DeSouza, and Cell Biology, 136 Harrison Ave, Bostc Location/Qualifiers
                                                                                                                                                                                                                                                                       An estrogen-dependent secretory protein, which shares identity with chitinases, is expressed in a temporally and regionally specific manner in the sheep oviduct at the time of fertilization and embryo
                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 2034)
DeSouza,M.M. and Murray,M.K.
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/clone_lib="sheep oviduct
/sex="female"
 /product-"estrogen
                                        17..78
                                                                                                                       organism="Ovis aries"
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                                                                                                                                                  gctgccgtctctggggacccccacgtcatccagaaagcatatgatgcacgccttctgggc
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                                                               CAGAACCTGGATTTTGTCAACCTTATGGCCTACGACTTCCATGGCTCTTGGGAGAAGGTC
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/translation="mckillawglllmlkhhdgaahklvcvftnwafsrpgsasilpr
/translation="mckillawglllmlkhhdgaahklvcvftnwafsrpgsasilpr
/translation="mckillawglldkilypefnklkernrglktllsvggwr
| translation="mckillawglldkilypefnklkernrglktllsvggwr
| dldpflcttlvfafasmnnqivpkdpldlefixlypelkrspakdrwtvfll
| efilqafkneaqltmkprlllsaavsgdphviqkaydarllgrlldfisvlsydlhgs
| wekvyghnsplstlpddpkssaxymglgvppklklglptigrtfilasgor
| lgagaagpaspgkymgqgflayyevgskkrwindgyvpyafkckwygyddba
| isfgykaffikrehfggamvwtldlddfrgnfcgtgpfplahtlnnllvndefsstps
| pkfwpfstavussridpemptwrdltmglgilplggeavatethksamwttprefaatprrfsvgrlavspggiavgphlgggkytpp
| atpirtplssgrtaapegktespgekpltsvgrlavspggiavgpvhlqigqkvtpp
| grkagypekytipsgkmtytpdgraetlerl"
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/product="estrogen dependent oviduct protein"
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1855..1860
2012..2017
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ampulla specific"
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Pred. No. 7.86e-65;
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                                                                                             ccccgggatctggacccctttctctgcacccacctggtatttgcctttgcctcgatgaac 159
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Reprod. Fert. Dev. 8
2 (bases 1 to 1596)
Marshall, J.T.A.
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Marshall, J.T., Brownlee, A.G. and
Cloning and sequencing of a cDNA
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Vertebrata; Eutheria; Artiodactyla; Ruminantia;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-DEC-1994) James T. A. Marshall, Division of Animal Production, Commonwealth Scientific and Industrial Research Organization, Locked Bag 1, Delivery Centre, Blacktown, New South Wales, 2148, Australia
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larity 58.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                  /note="derived from PCR primer based on bovine sequence: GenBank Accession Number D16639" complement(1575..1596)
/note="derived from PCR primer based on bovine sequence: GenBank Accession Number D16639" a 440 c 430 g 374 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPGKITKQAGELAYIEVCSFVQRAKKRWINDQYVPYAFKGKEWVGYDDAISEGYKAFF
IKREHFGGAMVWTLDLDDFRGNFCGTGPFPLVHTLNNLLVNDEFSSTPSPKFWFSTAV
NSSRIGPEMPTNTRDLTTGLGILPLGGEAVATETHRKSATMTTTPRGETATPTRTPLS
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STFSINRERFVNSVI ALLRTHGFDGLDLFFLY PGLRGS PARDRWIFVFLLEELLQAFKN
EAQLIMREPILLSAAVSGDHVI QKAYDARLLGRLLDE I SVLSYDLHGSWEKVTGHUS
PLFSLPGDPKSSAYAMSYWRQLGVPPEKLLMGLPTYGRTFHLLRASQNELGAGAVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="inferred from bovine sequence:
Number D16639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGRRTAAPEGKTESPGEKPLTSVGHLAVSPGGIAVGPVHLQIGQKVTPPGRKAGVPEK
VTTPSGKMTVTPDGRAETLERRL"
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/db_xref="PID:g602294"
/translation="LLLVLKHHDGAAHKLVCYFTNWAFSRPGSASILPRDLDPFLCTH
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Pred. No. 6.99e-61;
0; Mismatches 253;
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Regional Distribution and Hormonal Control of Estrogen-Dependent Oviduct Specific Glycoprotein mRNA in the Baboon (Papio anubis) Biol. Reprod. (1996) In press
                                                                                                                                             Submitted (05-MAR-1991) Randal and Biophysics, University of Chicago, IL 60612-7342, USA
                                                                                                                                                                                                                                                                                                                                                                                    Cloning of a recombinant complementary DNA to a baboon (Papio anubis) estradiol-dependent oviduct-specific glycoprotein Mol. Endocrinol. 5 (3), 356-364 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            estradiol-dependent oviduct-specific glycoprotein.
Papio hamadryas anubis cDNA to mRNA.
Papio hamadryas anubis
Papio hamadryas anubis
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Cercopithecidae;
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glycoprotein mRNA, partial cds.
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             /codon_start=1
/product="estradiol-dependent oviduct-specific
glycoprotein"
                                                                    /organism="Papio hamadryas
13..1884
/db_xref="PID:g1256951"
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                           acaggacataatagccccct 698
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DLDPFLCTHLIFAFASMNNOQIVAKDLODEKILYPETNKLKERNRELKTILSIGGNNF
GTSRETTMLSTFANREKFIASVISLLRTHDEDGLDLFEILYPGLRGSPHHDRWTFLFLI
EELLFAFKEALLTMRPRLLLSAAVSGVVHIVQTSYDVRFIGRLDFINVLSYDLHGS
WEKFTGHNSPLFSLPEDPKSSAYAMNYWRKLGAPSEKLLMGIPTYGRTFRLLKASKNG
LQATAIGPASPGKYTKOAGFLAYFEICSTWGAKKHWIDYVYYANKGKEWVGYDDA
ISFSYKAWFIJREHFGGAMYWTLDMDDYRGTFCGTGPPPLVYVNNDLIVRAFESSTSL
PQFWLSSAVNSSTDPERLAVTKAWTTDIKILPPGGEAGVTEIHGKCENMTITPRVTI
VTPTKETVSLGKHTVALGEKTELTGATTMTSVGHOSMTPEEKALTPVGHOSELPGKKT
LTPVGHQSVTTGQKTLISVGYHSTYPGEKTLTPVGHPSVTPVSHQSVSPGGMTMTPVH
FQTETLRQNTMAPRIKAVAHEKVTVPSRKISVTPEGQTVPLRGEYLTSETGTHPQDG"
59 a 572 c 531 g 566 t
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139 8

128

BASE COUNT ORIGIN

Matches

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485 499 425 439 365 379 305 319 245

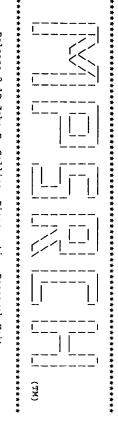
Search completed: Sun Jun Job time: 1542 secs.

29 19:55:25 1997

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> 605 619 545 559

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by Intelligenetics, Inc. ◻

MPsrch_nn n.a. • n.a. database search, using Smith-Waterman algorithm

9 Sun Jun 29 19:55:44 1997; MasPar time 175.81 Seconds 860.863 Million cell updates/sec

Tabular output not generated.

>US-08-663-618A-1 (1-1636) from US08663618A.seq

Description:
Perfect Score:
N.A. Sequence:
Comp: 1636

Scoring table: TABLE Gap 6 default

Nmatch STD Dbase 0; Query 0

121476 seqs, 46255616 bases ×

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.561; Variance 5.543; scale 1.725

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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15 16 17	10 12 14	987	554WDP	Result No.
3 3 3 5 6 6	38 37 38	51 45	178 133 93 92 85 78	Score
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12 12 12	12 12 12	15 9	13 15 15 2	BB
Q70465 Q70466 Q70473	Q51746 Q70468 Q70467 Q70469 N81164	Q90444 N81164 Q51746	Q85245 N81756 Q90443 Q10572 Q90442 Q10572	IJ
Generic DNA sequence Generic DNA sequence Generic DNA sequence	Oligonucleotide probe Generic DNA sequence Generic DNA sequence Generic DNA sequence Base substituted E.co	Hamster oviduct speci Base substituted E.co Oligonucleotide probe	YKL-40 gene. Gene encoding polypep Murine oviduct specif Human Natriuretic Pep Bovine oviduct specif Human Natriuretic Pep	Description
4.09e-07 4.09e-07 1.50e-06	1.37e-10 2.95e-08 1.11e-07 1.11e-07 2.95e-08	1.61e-27 4.79e-16 2.21e-12	7.87e-103 4.48e-71 1.67e-43 7.92e-43 4.11e-38 1.92e-33	Pred. No.

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154 acaccagctggtcccagtaccgggaaggcgatggggagctgcttcccagatgcccttgacc 213

CAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCTGCTGCAAAACTGGTCTGCTACT 83

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ALIGNMENTS

Query Match Best Local (Use of YKL-40 and anti-YKL-40 antibodies - for developing prods. for diagnosis prognosis and therapy of diseases involving connective tissue degradation.

Disclosure; Page 66-67; 88pp; English.

YKL-40 (40 KDa) was purified from human osteosarcoma MG63 cells.

The N-terminal sequence is shown in R70745; the full coding region of the YKL-40 gene is given in Q8245. Homology of the N-terminal and 2 internal peptides (R70746-47) with a bacterial polysaccharide hydrolase suggests that YKL-40 degrades polysaccharide components of connective tissue. YKL-40 is a marker of e.g. metastatic breast cancer and inflammatory or degenerative joint diseases.

Sequence 1681 BP; 401 A; 503 C; 421 G; 356 T; 19-JAN-1995. 08-JUL-1994; 09-JUL-1993; OR5245 standard; cDNA; 1681 BP. 085245;
085245;
12-AUG-1995 (first entry)
YKL-40 gene.
YKL-40; diagnosis; prognosis; therapy; breast cancer; metastasis;
marker; joint disease; connective tissue; ss. (REGC) UNIV CALIFORNIA. Johansen JS, Price PA; WPI; 95-066866/09. /*tag= a WO9501995-A. Homo sapiens. 10.9%; 1 Similarity 63.6%; 698; Conserva+4 U07754. US-089989. Location/Qualifiers 135..1681 Score 178; DB 13; 1 Pred. No. 7.87e-103; 0; Mismatches 376; Length 1681;

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J63039-A.
30-JAN-1988.
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16-JUL-1986; JP-167518.
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J07107979-A.
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15-AUG-1994;
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Disclosure; p; Japanese.
Polypeptide encoded is involved i response, cell growth and activat Sequence 966 BP; 238 A; 282
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Gene encoding polypeptide involved :
Immune response; cell growth; ss.
Key
Location/Qualifiers
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1..966
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Murine oviduct specific glycoprotein;
Murine oviduct specific glycoprotein;
MOGP; ds.
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Q10572;
Q10572;
Q109-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure;
hyperaldosteronism; glaucoma; guanyl
            Peptide
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding an oviduct-specific glycoprotein - useful recombinant protein production in high quantities. Claim 1; Pages 11-14; 22pp; Japanese. O90443 encodes R73992 murine oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. MOGP in high quantities. Sequence 2504 BP; 678 A; 616 C; 538 G; 672 T;
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Similarity 58.7%;
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Best Local S
Matches 10
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22-JUN-1999; U03586.
23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M. Goeddel D. Lowe
WPI; 91-036711/05.
                                                                                                                                                                                                                                                                                                                                                                                            Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce MPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                     also be prepd.
Sequence 1047 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= N-glycos_site
w09100292-A.
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Modified -site 35..37
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Modified -site 161..163
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d -site 277..279
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d -site 244..246
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New DNA encoding an erecombinant protein prot
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19-AUG-1993; JP-227881.
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oviduct-specific glycoprotein production in high quantities. 22pp; Japanese.
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                     Domain
/label=
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Q10572 standard; DNA; 1047 BP.
Q10572;
Q10576;
Q10578-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure;
                                                                                                                                    Protein
/label=
                                                                                                                                                                              Peptide
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Sequence 1994 BP; 445 A; 536 C; 520 G; 493 T;
                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                     hyperaldosteronism; glaucoma; guanyl
                                          /label= extracellular domain
/note= "binds natriuretic peptides
Domain 456..456
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
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Modified -site 277..?
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Modified -site 244..246
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Modified -site 195..197
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/label N-glycos_site
Modified -site 35..3
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/odified -site 600...
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/odified -site 161..163
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scdktnnstnanvangtgntnnmngvssnnnnrknmnnknnasmnwrnrwnnnnngnsnr
                               CCTGGCAGAACGTGTCTTGTCCAGGGCTGGGGCCCATGCTCAGGTTCAGAGGGCTGACCTG
                                                                                                                        nsnmnnnagcnydgnnnyanvnnntnnnggtrndgnrnvnkmngrryhgvtgnvvmdknn
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                                                            drntdnvnwamgdndsgdnnnaahysganknnwwtgrnnnwvkgannsdnnncandnddn
                                                                                            CTGCACAGCTGTAGAAGCTGGACCGTTCCCGAGGATTGGGATAGAGCCCATCAGCTTTGC
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                                                                                 Query Match
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Matches 23
                                                                                                                                                                                       New DNA encoding an oviduct-specific glycoprotein - useful frecombinant protein production in high quantities. Claim 1; Pages 16-18; 22pp; Japanese. 090444 encodes R73993 hamster oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. c HOGP in high quantities. 574 C; 573 G; 617 T;
                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-1995.
15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO
WPI: 25-190179/25.
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Matches 1
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E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are completed to forms that can amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of wh
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05-MAY-1988.
30-MAR-1988;
03-APR-1987;
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(SUSO) SUOMEN SOKERI OY.

Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikaine
MPI; 88-279927/40.

Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer
minimum and stranded template and screening.
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                                                                                              n 3.18;
Similarity 15.48;
18; Conservative
                                                                                                                                                                                               singularly in any given mutant. p80575. 21 A; 47 C; 17
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uted E.coli beta-galactosidase alpha-fragment.
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62; N
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l. No. 4.79e-1;
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Q51746 standard;
Q51746;
31-MAY-1994 (fir
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Q51746;
31-MAY-1994 (fir
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Shank DD, Spears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes
detection and amplification
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01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1993;
24-MAY-1993;
26-MAY-1992;
                                                                                                                                                                oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                 samples
Claim 3;
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Oligonucleotide probe MK14-A consists of nucleotides 5-95 (Q51735). It hybridized to all spp. of mycobacteria test cross reacted to a few non-mycobacterial spp. The probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
EP-571911-A.
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CCTGCCCAAGGACTTGGACCCCAGCCTTTGCACCCACCTCATCTACGCCTTC
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probe MK14-A
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Pred. No.
47; Misma
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. 1.37e-10;
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2.21e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins PT comprising a binding domain and an effector domain PS Disclosure; page 35; 255pp; English.

CC 070468 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be CC represented as follows: x(NB)11(TGC)(NNB)5Z(NNB)7(TGC)(NNB)10Y: x CC and Y are flanking restriction sites (X is not the same as Y) that are CC not specified further. Other generic sequences are shown in Q70466-68.

CC Other specified further. Other generic sequences are shown in CC comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is CC chemically or biologically active. They may further comprise a linker CC peptide between the 2 domains. The oligonucleotides are also designed so CC that the expressed peptide contains 2 or 4 cysteine residues positioned CC in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs CC compsns. comprising a TSAR binding domain can be used in vivo to CC deliver a chemically or biologically active moiety, eg. metal ion, CC cell. They can also replace the function of macromoleules, eg.

CC monoclonal or polyclonal antibodies and therefore circumvent the need CC cell. They can also replace the function of macromoleules, eg.

CC monoclonal or polyclonal antibodies and therefore circumvent the need CC callowing direct and rapid detection in a screening process.

Squence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
                             LT 12
Q70467 standard; DNA; 114 |
Q70467;
O5-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NORTH C. Fowlkes DM, Kay BK; WPI; 94-279739/34.
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Q70468;
Q5-APR-1995 (first e
Generic
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DNA sequence to generate a
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5, 9 or 12 nucleotides (see
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4.5%;
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Pred. No.
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random TSAR petide library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins proteins or peptides and an effector domain proteins processing a binding domain and an effector domain proteins are comprising a generic DNA sequence used to generate random TSAR (Totally CS ynthetic Affinity Reagents) peptides. This generic formula can also be crepresented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)11 X X CC and Y are flanking restriction sites (X is not the same as Y) that are contained the terofunctional proteins or peptides other specific peptides generic sequences are shown in Q70466-68. CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain that is CC peptide between the 2 domains. They may further comprise a linker CC peptide between the 2 domains. The oligonucleotides are also designed so CC that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs CC comprise a chemically or biologically active moiety, eg. metal ion, cc deliver a chemically or biologically active moiety, eg. metal ion, cc call. They can also replace the function of macromolecules, eg. cc complex methods of hybridoma formation or in vivo antibody production. CC complex methods of hybridoma formation or in vivo antibody production. CC complex methods of hybridoma formation and activity allowing CC direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                  Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do effector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                Q70469 standard;
Q70469;
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                                misc_feature
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Synthetic.
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                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGAGGCTCGCTTCCTGCCCAAGGACTTGGACCCCAGCCTTTGCACCCCACCTCATCTA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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6, 9 or 12
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                                                                                                                                                                                                                                                                                                                                                    DNA;
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12 nucleotides (see
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                                                                                                                                                                                                                                                                                                                                                    114 BP.
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Pred. No. 1.11e-07;
32; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can
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"this sequence represents '2'; 2 can se of 6,9 or 12 nucleotides (see

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RESULT ACCOUNTS ACCOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC Q70469 is a generic DNA sequence used to generate random TSAR peptide CC Q70469 is a generic formula can be represented as follows: X(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)14(TGC)X: X and Y are flanking restriction CC sites (X is not the same as Y) that are not specified further. This CC sequence generates peptides that are cloverleaf in structure. Other CC generated by these generic sequences are shown in Q70465-68. Other specific peptides CC generated by these generic sequences are shown in R65150-54. TSARs are CC concatenated heterofunctional proteins or peptides, comprising at least CC two functional regions - a binding domain with affinity for a ligand and CC a second effector peptide portion that is chemically or biologically CC active. They may further comprise a linker peptide between the 2 domains. CC The oligonucleotides are also designed so that the expressed peptide CC contains 2 or 4 cysteine residues. These residues confer some degree of CC conformational rigidity to the peptides. The TSARs or compsis. comprising CC a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma or in vivo annihologue of hybridoma are easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUGO) SUDMEN SOKERI OY.
Lehtovaara P, Knowles J, I
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18-AUG-1994; U00977.
01-FEB-1994; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROL.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                  08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                      /*cag- b
EP-285123-A.
                                                                                                                                                                                     primer_bind
/*tag= b
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screening a recombinant vector library expressing fusion
comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English
                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                               /function-multiple cloning 187..204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    formation or in vivo antibody production.
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                                                                                                                                                                                                                                                                                                          Location/Qualifiers 19..69
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                                                                                                                                                                                                                                              cloning site
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   Koivula A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 12;
Pred. No. 1.11e-07
32; Mismatches 7;
   Bamford J, Reinikainen
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PD 18-AUG-1994; U00977.

PF 01-FEB-1993; US-013416.

PR 01-FEB-1993; US-013416.

PR 30-DEC-1993; US-013416.

PR 30-DEC-1993; US-013416.

PR 30-DEC-1993; US-013416.

PR 30-DEC-1993; US-0189331.

PA (UVNC-) UNIV NORTH CAROLINA.

PA (UVNC-) UNIV NORTH CAROLINA.

PI FOWLKES DM, Kay BK;

DR P-SDB; R65150 and R65151.

PR P-SDB; R65150 and R
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Best Local :
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Random point mutations were introduced into the alpha fragment of E. coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 15
Q70465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding d effector domain; concateneated heterofunctional protein; linke direct; rapid; detection; screening; treatment.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 27 16:52:08 1997; MasPar time 11.66 Seconds 435.449 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score:

Sequence: >US-08-663-618A-2 (1-466) from US08663618A.pep 3443 1 MVRSVAWAGEMVLLMIPWGS......QQSCPTGLVFSNSCKCCTWN 466

Scoring table: PAM 150 Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 36.077; Variance 158.164; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	71
1 2 3 3 3 3 3 3 4 4 4 3 3 3 3 3 3 3 1 1 1 1	Result
1350 1345 1325 912 917 597 597 581 576 576 576 576 576 213 389 389 313 313 913 99	Score
39.2 38.1 117.3 116.5 7.9 116.7 116.7 110.3 110.3 110.3 110.3 110.3 110.3 110.3 110.3	Query Match
668 7537 713 3211 371 371 371 389 423 423 423 866 561 256 255 256 256 256 256 256 256 256 256	Length
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R73993 R73992 R73992 P81342 P81342 R70025 R70029 R56861 R56861 R330072 R330072 R330078 R348981 R44823 R464823 R464823 R707451 R707451 R707451 R707451 R707751	ID
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2.13e-115 1.14e-115 1.17e-13 3.09e-73 2.36e-43 2.36e-43 7.47e-42 2.20e-41 9.94e-41 9.94e-41 7.19e-31 1.55e-22 1.55e-23 1.79e-02 1.79e-02 3.04e-02 3.04e-02 1.58e+01	Pred. No.

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P50319	R90772	R98125	R99248	R87724	R94503	R92750	P50017	P70423	P50018	R36735	R32904	R07311	R47264	R88058	R97235	R70746	R70752	R26999	R47259	R21521	P81181	R07575	R80445	******
Human antihaemophilic	Bacillus stearothermo	Human lymphocyte cell	Limnanthes 2-acyltran	Full length meadowfoa	1-acylglycerol-3-phos	Human EGF receptor su	Sequence encoded by t	-	Sequence encoded by t	Human BMP-6.	Human BMP-6 peptide s	Human Bone Morphogene	Pre-pro BMP6.	Protein encdoed by Mu	MuTu putative oncogen		l per	Novel type III RTK en	Pre-pro-VGR1.	Alpha galactosidase.	Sequence of glucoamyl	Glucoamylase encoded	Murine soluble epoxid	HIGH HIS DIE V.
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Best Local S
Matches 19
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N-PSDB; 200442.

New DNA encoding an oviduct-specific glycoprotein recombinant protein production in high quantities. Claim 4; Pages 7-9; 22pp; Japanese.

Q90442 encodes R73991 bovine oviduct specific glycoprotein converses the commercial recombinar BOGP in high quantities.

Sequence 537 AA;
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/label- mat_p
J07107979-A.
25-APR-1995.
15-AUG-1994;
19-AUG-1993;
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Bovine oviduct specific gl
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  J63032898-A.
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ULT 4
P81342 standard; protein; 3;
P81342;
19-OCT-1990 (first entry)
Polypeptide involved in prot
Immune response; cell growt)
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New DNA encoding an oviduct-specific glycoprotein - useful process of the production in high quantities.

Claim 4; Pages 11-14; 22pp; Japanese.

Q90443 encodes R73992 murine oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn.

MOGP in high quantities.

Sequence 718 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO
WPI; 95-190179/25.
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Murine oviduct specific glycoprotein.
Murine oviduct specific glycoprotein;
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R73992 standard;
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                                                                                                                        FSCNQGRYPLIQTLRQELSLPYLPSGTP
                                                                                                                                                                                                 TYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQ
                                                                                                                                                                                                                                                                                                                                                                             tfcgngpfplvhil-nellvgtesnstp
                                                                                                                                                                                W-KGATKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAG
                                                                                                                                                                                                                                           QWLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCS
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   growth
                 protective
                                                             321
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Pred. No. 1.17e-113;
81; Mismatches 107;
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16-JUL-1986; JP-167518.
(DAIN) Dainippon Pharm K
WPI: 88-068419/10.
P-PSDB; P81342.
New plant protein having endo-chitinase activity - used in antifungal compsns. and to develop transformed plants which are less susceptible to fungal infection.
Claim 3: Page 19-20; 43pp; English.
Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN tobacco plants with a probe derived from PROB40 (a partial Cluster-A cDNA clone) resulted in the isolated of 11 positively hybridising clones. Analysis revealed that all were identical and corresp. to Cluster-A cDNA. The nt sequence of clone cA-3 is given in Q82973/R70025. This clone lacks 7 codons of the 5' part of the ORF. The cDNA clone was completed by performing a PCR reaction on clone cA-3 with primer T7 (082794) and primer P1 (Q82975). A partial AA sequence of the protein isolated from TMV-infected tobacco leaves
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This polypeptide is involved in protective mechanisms such as response, cell growth and activation of protective functions. Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                         Apotheker-de Groot M,
Melchers LS, Ponstei
                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1993; 202425.
17-AUG-1993; EP-202425.
(MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
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                                                                                                                                                                                                                                                                                                                             N-PSDB; Q82973
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95-083454/12.
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'---'~ transformed plants which
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Sela-buurlage
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Pred. No. 3.
65; Mismatc
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fungicide; Cluster-A.
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New plant protein having endo-chitinase activity - used in antifungal compans. and to develop transformed plants which are less susceptible to fungal infection.

I less susceptible to fungal infection.

Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN tobacco plants with a probe derived from PROB40 (a partial Cluster-A cDNA clone) resulted in the isolated of 11 positively hybridising clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to closes. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clones. Analysis revealed that all were identical and corresp. to clone ca. 3 is given in 082973/CC R70025. A genomic library of N. tabacum was screened using the cluster-A cDNA including the deduced primary structure of the Cluster-A cDNA including the deduced of the cDNA complete int. sequence of Cluster-A cDNA including the deduced of the cDNA complete int. sequence of Cluster-A cDNA including the deduced of the cDNA complete int. sequence of Cluster-A cDNA including the deduced complete int. sequence of Cluster-A cDNA including the deduced complete int. sequence of Cluster-A cDNA including the deduced complete int. sequence of cluster-A cDNA including the deduced complete int. sequence of cluster-A cDNA i
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(UVILE-) RIJKSUNIV LEIDEN.
Apotheker-de Groot M, Bol
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                                                                                                                             Fusarium,
Erysiphe,
Sequence
                                                                                                                                                 Example 8; Page 45; 62pp; English.

Q78144 encodes R63441 the Trichoderma harzianum pl endochitinase, which can be used to inhibit chitin containing fungi and chitin containing herbivorous insects, especially from the genera below containing herbivorous insects, especially from the genera below preservium, Gliocladium, Rhizoctonia, Trichoderma, Uncinula, Ustilage,
                                                                                                                                                                                                                                                                                                                                            Trichoderma harzianum
                                                                                                                                                                                                                                                                                                                                                        chitin
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Trichoderma harzianum
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14-APR-1993; US-045:
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107; Conse
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424 AA;
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                                                                                                                                                                                                                                                                                                                                                                      The sequence coding for wheat germin, a protein induced during germination of wheat, is a preferred example of DNA coding for a protein able to degrade oxalic acid. Such DNA can be coupled to sequence of interest, e.g. one coding for enzymes which confer resistance to pathogens (esp. endochitinases). Plant calli which have been successfully transformed by the sequences are selected by their ability to grow on oxalic acid-contg. medium. R56861 is a known sequence of a mature endochitinase; the sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell selection, esp. gene coupled to gene-encoding conferring pathogen resistance Disclosure and Claim 8; Page 39-40; 64pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grezes-Besset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= endochitinase
WO9413790-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen resistance; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxalic acid degradation; oxalate (filamentous fungus endochitinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R56861 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of gene encoding oxalic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q68353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SNEI) ELF SANOFI.
(ERAP) SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aphanocladium album mature endochitinase.
                                                                                                                                                                                                                                                                                                                                                          previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aphanocladium album.
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                                                                                                                                                                                                                                                                                Local Similarity
mes 101; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              svaqayysydpsskelisfdtpdmintkvsylknlglggsmfw
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gcysydpstkelisfdtpamistkvswlkgkglggsmfw
                                                     lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak 305
                                                                                                            kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv 253
                                                                                                                                                      GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                                                                                                                                                                                                               lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEV
                              LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                          QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                                                                                  -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-lg 194
                                                                                                                                                                                                                    LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 142
                                                                                                                                                                                                                                                                                                                                             disclosed in EP-531218. 389 AA;
                                                                                                                                                                                                                                                                              16.7%;
larity 36.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxalate oxidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ic acid degrading coupled to gene-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell selection
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Pred.
65; M
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                                                                                                                                                                                                                                                                              e 576; DB 10; 1
. No. 2.20e-41;
Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selection
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                                                                                                                                                                                                                                                                                                           Length
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VPYIF-RD-NOWVGFDDVESFKTKVSYLKQKGLGGAMVW

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Best Local S
Matches 10
R33068;
30-JUN-1993 (first
Aphanocladium album
                                   R33068
                                                                                                                                                                                                                                                                                                                                                                                    mRNA by screening with anti-chitinase antiserum. Three probes were designed based on the CH3C sequence, corresponding to the start, middle and downstream regions of the coding sequence. The probes were used to isolate the full-length coding sequence of A.album endochitinase from an A.album cDNA library in PTZ19R. A 1.6kb fragment was identified in serval positive clones. The sequence of the fragment contained an ORF encoding a 423 amino acid protein. The mature endochitinase can be used to control pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SNFI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protecting plants against fungi, insects, etc. Claim 1; Fig 1; 75pp; French. Clone CH3C was isolated from a cDNA bank prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blaiseau P, Legou
WPI; 93-078700/10.
N-PSDB; Q37711, Q3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-1992; 402414.
06-SEP-1991; FR-011072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1993 (first entry)
Aphanocladium album pre-pro-e
filamentous fungus; pathogen
Aphanocladium album.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R33072 standard;
R33072;
                                                                                                                                                                                                                                                                                                                                                                              such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA encoding fungal endo:chitinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                        340
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                                                                                                                                                                                                                                                                                  lkkqnrnmkvmls1ggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp
                                                                                           gcysydpstkelisfdtpamistkvswlkgkglggsmfw 378
                                                                                                                                                                                       LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
                                                                              VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                        GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                           QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                              LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                                                                                                                                                                                                                                                    101;
                                                                                                                                                                                                                                                                                                                                                                 fungi,
se 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 23..34
"pro-sequence"
n 35..423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "pre-sequence"
23..3
                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                                                                   h 16.7%;
Similarity 36.2%;
101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endochitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legoux R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q37712.
                                   Protein;
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            entry)
  mature
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  endochitinase
                                                                                                                                                                                                                                                                                                                Score 576; DB 6;
Pred. No. 2.20e-41;
65; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance.
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                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                        Length 423
                                                                                                                                                                                                                                                                                                                   Indels 18;
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                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT RE
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Best Local :
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Chitin biosynthetic enzymes end I, exo I and exo II - are periplasmic chito; dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl; sluco; amidase(s), respectively example 4; Page 79-82; 101pp; English. Periplasmic chitodextrinase (W02156), periplasmic Periplasmic chitodextrinase (W02157) and aryl Beta-N-acetylglucosaminidase (W02158) can be used to produce chitin oligosaccharides with the structure (GlcNAc)n where n is 2 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA encoding fungal endo:chitinase - useful for protecting plants against fungi, insects, etc. Claim 22; Page 60-61; 75pp; French.

This mature protein from the filamentous fungus Aphanocladium album has endochitinase activity and is used to control patho;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 11
W02159
                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1996; U02332.
13-FEB-1995; US-386727.
(UYJO) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      album has endochitinase activity and is used to control paths such as fungi, bacteria, arthropods and nematodes on plants. Recombinant DNA comprising the endochitinase coding sequence specifically intended for transforming Nicotiana tabacum, Heigher Comprised to the control of the control o
                                                                                                                                                                                                                                                                                                                                                          Yu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Periplasmic chitodextrinase;
Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 93-078700/10.
N-PSDB; Q37704.
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                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9625424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SNFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
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                                                                                                                                                                                                                                                                                          96-393335/39.
DB; T36390.
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Pred. No. 9.94e-41
66; Mismatches 9
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chitin; oligosaccharide; catabolic;
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all genes
Sequence
                                                                                                                                                                                   Plant cell conty. signal sequence of chitinase A gene - for secretion of foreign polypeptide, esp. chitinase A for protection against pathogenic fungi and nematodes. Disclosure; Fig. 1A-1C; 20pp; English. Serratia marcescens QMB1466 genomic DNA was partially digested, liquited into vector pLAFRI, packaged into lambda phage particles, and used to transfect Escherichia coll DH1 (ATCC 33849) cells. Plating on chitin medium was used to screen for chitinase activity. Clone C12 (ATCC 67152) was isolated. Its sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R64823 standard; Protein; 561 R64823;
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09-JUL-1990;
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R-1984; US-593691.

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DAN PLANT TECHNOLOGY C
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93; Conse
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No. 4.43e-24;
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ace in R64823
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tively. They are
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Best Local S
Matches 8
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01-MAR-1984; 593691.
26-MAR-1984; US-593691.
26-MAR-1986; US-888033.
18-JUL-1986; US-888033.
09-JUL-1990; US-550253.
14-AUG-1992; US-930970.
(DNAP ) DNA PLANT TECHNOLOGY COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibition of chitinous fungal plant pathogens - by transforming plant with DNA encoding chitinase activity
Disclosure; Fig.1; 13pp; English.
Plasmid pCHIT1251 containing the chitinase-A gene (chiA), fused directly to a nos promoter, may be used to transform, via Agrobacterium sp., a crop plant. The resulting transgenic plants expressing the chitinase-A protein fragment are protected against fungi, nematodes, insects and disease agents. The protein is preferably expressed by the plant only at the site of pathogen attack, e.g. only in the root cells. The plants express the chitinase in a biologically active form.

Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 94-074348/09.
N-PSDB; Q57966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial chitinase-A fragment from pCHIT1251. Chitinase-A; enzyme; transgenic plant; biological condisease-resistance; crop improvement; Agrobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287
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EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KVTGHNS 226
                                                                                                                                                                                                                                                                               AFAGMTNHQLSTTEWNDE-T-LYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATAN 114
                                                                                                                                                                                                                                                                                                                           pfaalqkaqkgvtawddpykgnfgqlmalkqahpdlkilpsiggwtlsdpfff-mgdkvk 289
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                                                                                                                                                                                                                           -rdrfvgsvkeflqswkffdgvdidwefpggkganpnlgspqdgetyvlvmkevgamldq 348
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
89; Conse
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larity 27.6%;
Conservative
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pgsrhrlhhgegrecaagggvkpgkivvgtamygrgwtgvngyqnnipftgt
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Pred.
84; M
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                                                                                                                                                                                                                                                                                                                                                                                                e 372; DB 9; Le
. No. 1.56e-22;
Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          561;
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RESULT
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Best I
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                                                                                                                                                   W09625424-A1.
22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 51pp; English.

The sequence is that encoded by the Heliothis armigera (Ha) nuclear polyhedrosis virus (NPV) immediate early-1 (IE-1) g(partial sequence).

Sequence 238 AA;
                                                             Yu C;
                                                                                                                                                                                                                                                                14-JAN-1997 (first entry)
Periplasmic chitodextrinase.
Periplasmic chitodextrinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 14
R32547 standard;
                                                                               13-FEB-1996; U02332.
13-FEB-1995; US-386727.
(UYJO) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insect virus with reduced capacity to occlude for controlling proliferation of insect pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q35982
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Christian PD, Dall DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1992;
05-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heliothis armigera WO9303144-A. 18-FEB-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heliothis armigera nuclear polyhedrosis virus; insecticide; immediate early-1.
                                                                                                                                                                                                                                             Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                W02156 standard;
W02156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmission
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HaNPV IE-1 gene protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
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                                                                                                                                                                                                                                                                                                                                                                                                                                  224 HNSPLYKRQEESGAAASLNVDAAVQQWL-QKGTPASKLILGMPTYGRSFT
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Local
                       96-393335/39.
DB; T36387.
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AFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVT-G
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biosynthetic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 7.9%;
Similarity 34.1%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU0413.
AU-007576.
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                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nuclear polyhedrosis virus
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                                                                                 Keyhani
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  end
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chitin; oligosaccharide; catabolic;
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43; M
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1. No. 1.65e-1
Mismatches
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Hanzlik TN,
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  and
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                                                                                                                                                                                                                                             periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) aryl beta-N-acetyl:gluco:amidase(s), respectively Claim 2; Page 68-71; 101pp; English.
Periplasmic chitodextrinase (W02156), periplasmic Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02158) can be used to produce chit oligosaccharides with the structure (GlcNAc)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes endI, exoI and exoII respectively. They are all genes involved in the catabolic pathway of chitin.
                                                                                                                                                                                                                                  Sequence
                                                                                                                 514
                              573
 225
                                                           168
                                                                          ekldvasaqdgvhymltiaapss-ayllrgmetmavtqyldyvnimsydlhgawndhvgh 572
                  naalydtgkdselagw-nvygtag
                                                         QEAQ-TSGKE--RLLLSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGH
 NSPLYKRQEESGAAASLNVDAAVQ
                                                                                                                                                                                          Similarity
                                                                                                                                                                             48;
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33.3%;
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d. No. 5.16e-09;
Mismatches 42;
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Search completed: Fri Jun 27 16:54:04 1997 Job time: 116 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fr1 Jun 27 16:49:12 1997; MasPar time 21.48 Seconds 618.601 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-663-618A-2 (1-466) from US08663618A.pep 3443 1 MVRSVAWAGEMVLLMIPWGS......QQSCPTGLVFSNSCKCCTWN 466

Scoring table:

PAM 150 Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir50 1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 48.408; Variance 102.872; scale 0.471

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	3	42	41	40	39	38	37	36	ა 5	34	33	32	31	30	29	28	27	26	25	24	23	22
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alpha-glucosidase (E		glucan 1,4-alpha-glu	н	retrovirus-related p	retrovirus-related c	probable membrane pr	umuC protein - Esche	probable coproporphy	_	homologies with orf	chitinase (EC 3.2.1.	chitinase (EC 3.2.1.	oviduct-specific sia	oviduct-specific gly	estradiol-stimulated	39K whey protein - b	chitinase (EC 3.2.1.	chitinase (EC 3.2.1.	RF2 protein - yeast	47K glycoprotein - f	chitinase (EC 3.2.1.	probable membrane pr	chitinase (EC 3.2.1.
2.17e+00	2.17e+00	2.17e+00	2.17e+00	7.49e-01	7.49e-01	1.67e+00	9.80e-01	9.80e-01	1.90e-01	1.08e-01	8.07e-03	8.07e-03	8.32e-05	8.32e-05	5.52e-10	5.52e-10		9.11e-22	1.29e-24	4.02e-25	.06e-	2.24e-33	2.06e-37

ALIGNMENTS

Oy 8 AGFMVLLMIPWGSAAKLVO Db 68 twewndvtlygmlntlkn	Query Ma Best Loc Matches	83 #leng	#cross-references MUID:90328983 #accession \$10677 ##molecule_type protein ##residues 22-40,'x',42-45 ##label NY2 KEYMORDS cartilage; extracellular protein; FEATURE	##residues 1-383 ##label ##cross-references GB:M80927 REFERENCE \$10677 #authors Nyirkos, P.; Golds #journal Biochem. J. (1990) #title Human synovial cel	on tus ecule_	TITLE TOTAL A49562 #type compl ALPERNATE_NAMES 39% synovial protein ORGANISM #formal_name Homo sapi DATE 03-Mar-1995 #sequence_ 03-May-1996 ACCESSIONS A49562; S10677; A33162 REPERENCE A49562 Republic Hakala, B.E.; White, C #journal J. Biol. Chem. (1993)
	%; Score 1519; DB 13; Length 383; 3%; Pred. NO. 8.84e-265; /e 88; Mismatches 83; Indels 9; Gaps	#domain signal sequence #status predicted #label SIG\ #product cartilage glycoprotein gp39 #status predicted #label MAT #length 383 #molecular-weight 42613 #checksum 2942	328983 'X',42-45 ##label NY2 extracellular protein; glycoprotein	1-383 ##1abel HAK erences GB:M80927 S10677 NyIrkos, P.; Golds, E.E. Biochem. J. (1990) 269:265-268 Human synovial cells secrete a 39 kDa protein similar to a bovine mammary protein expressed during the non-lactating	man cartilage gp-39, a major secretory product of arti- chondrocytes and synovial cells, is a mammalian member chitinase protein family. 9562 preliminary pe mRNA	A49562 #type complete cartilage glycoprotein gp39 precursor - human 39K synovial protein #formal_name Homo sapiens #common_name man 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 03-May-1996 A49562; S10677; A33162 A49562; S10677; A33162 Hakala, B.E.; White, C.; Recklies, A.D. J. Biol. Chem. (1993) 268:25803-25810

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ldlddfrgnfcgqnlrfpltsaikdvla 381
                   LAYYEVCSW-KGATKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWA
                                                                                                                                                                                                                                                                                      Similarity
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larity 51.0%;
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# #length 381 #molecular-weight 43001
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BRP39 protein - mouse
#formal_name Mus musculus #common_name house mouse
10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
03-May-1996
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BRR39 protein - mouse
#formal_name Mus musculus #common_name house
02-Jul-1996 #sequence_revision 02-Jul-1996 #t
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Oncogene (1994) 9:3417-3426
neu and ras initiate murine mammary
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Pred. No. 6.73e-253;
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FICATION #superfamily Streptomyces
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94; Mismatches 112;
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#accession I46470
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Similarity 48.8%;
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estrogen dependent oviduct protein precursor -
#formal_name Ovis orientalis aries, Ovis ammon
#common_name domestic sheep
16-Aug-1996 #sequence_revision 16-Aug-1996 #tex
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Endocrinology (1995) 136:2485-2496
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1-539 ##label DES
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Pred. No. 1.58e-233;
85; Mismatches 106;
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535 #checksum 2
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#length 537 #checksum 1695
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##residues 1-537 ##label
##molecule_type
           ##status
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l Similarity 50.4%;
191; Conservation
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Purification and molecular cloning of bovine oviduct-specific glycoprotein.
S57197
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chitinase
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S57197
                   Isolation, cloning,
stored in active i
A53918
                             Krishnan, A., Nair, P.N., Jones, D.
J. Biol. Chem. (1994) 269:20971-20976
Isolation, cloning, and characterization of new chitinase
stored in active form in chitin-lined venom reservoir.
                                                                                   #formal_name Chelonus
28-Jul-1995 #sequence_
03-May-1996
A53918
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28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
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oviduct-specific
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(EC 3.2.1.14) precursor -
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Pred. No. 2.27e-230;
80; Mismatches 101;
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#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:1548-1552
#title Transmission-blocking antibodies recognize microfilarial chitinase in brugian lymphatic filariasis.
#cross-references MUID:92179220
#accession A38221
                                                                                                                                                                                                                                 ##molecule_type nucleic acid; protein
##residues 1-50/ #...
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1 Similarity 42.8%;
158; Conservation
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l Similarity 42.3%;
159; Conservative
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                                                                                                                                                                          sequence extracted from NCBI backbone
glycosidase; hydrolase
#length 504 #molecular-weight 55971 #che
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#length 483 #molecular-weight 52013
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Pred. No. 7.24e-199;
100; Mismatches 100;
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Pred. No. 1.1
94; Mismatcl
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. No. 1.85e-179;
Mismatches 102;
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#accession A565
      372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status preliminary
##molecule_type mRNA
##residues 1-554 ##label KRA
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                                                                                                    QWLQKGTPASKLILGMPTYGRSFTLASSSDT-RVGA--P-ATGSGTPGPFTKEGGMLAYY 304
                                                                                                                               lweekgcpsnklvvgipfygrsftlsagnnnyglgtfinkeagggdpapytnatgfwayy 311
                                                                                                                                                                    TYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQ
                                                                                                                                                                                       SFDGLDLDWEYPGS--QGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQ
                                                                                                                                                                                                                                                                                                     N-DETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKY 130
                                                                                                                                                                                                                                                                                                                                                                     IPWGSAAKLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTN-H-Q-LST-TEW 71
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                                    EVCS--WKG-A--TKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPAS
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Similarity 38.8%;
162; Conservative
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Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinases of Manduca sexta.

CCS_MUID:93357793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycosidase; hydrolase
#length 554 #molecular-weight 62203 #checksum
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chitLinase (EC 3.2.1.14) - tobacco hornworm
#formal_name Manduca sexta #common_name tobacco
11-aug-1995 #sequence_revision 11-aug-1995 #text
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; Pred. No. 1.04e-168;
105; Mismatches 126;
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Best Local S
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#accession A383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                             309 W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL 360
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##cross-references EMBL:X78325
             ##molecule_type mRNA
##residues 1-378 ##label_HEI
                                                                                                                                                                                                                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261
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##cross-references GB:J05599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| || ||:|||:::||| : :|:|| || || : | ||||:|||:|||:||| 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 20.3%;
l Similarity 40.1%;
119; Conservative
                                                                      Heitz, T.; Segond, S.; Kauffmann, S.; Geoffro, V.; Brunner, F.; Fritty, B.; Legrand, M. Mol. Gen. Genet. (1994) 245:246-254
Molecular characterization of a novel tobacco pathogenesis-related (PR) protein: a new pla
                                                                                                                                                                                                       ss1591 #type complete chitinase (EC 3.2.1.17) P2 pathogenesis-related - common tobacco #formal_name Nicotiana tabacum #common_name common 15-Jul-1995 #sequence_revision 08-Sep-1995 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. (1990) 265:15659-15665
Gene cloning of chitinase Al from Bacillus circulans
revealed its evolutionary relationship to Serratia
chitinase and to the type III homology units of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #superfamily fibronectin type III repeat homology
glycosidase; hydrolase
#length 699 #molecular-weight 73677 #checksum 6
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                                                                                                                                                                               S51591; S51632; S43119
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chitinase (EC 3.2.1.14) precursor -
#formal_name Bacillus circulans
28-Jun-1991 #sequence_revision 28-Ju
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chitinase/lysozyme.
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Pred. No. 2.46e-104;
73; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oyanagi,
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##molecule_type protein

##residues 31-36;87-112;252-275;282-305;337-371 ##label HEW

#SSIFICATION #superfamily Streptomyces chitinase chi40

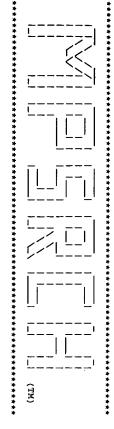
#SSIFICATION #superfamily Streptomyces chitinase chi40
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                              112
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##residues
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qlfk-lkkanrnlkvmlsiggwtwst-nfpsaastdanrknfaktaitfmkdwgfdgidv
| |: || | | :| :| :| :| | | ::| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: :|| |:: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDVESFKTKVSYLKQKGLGGAMVW
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                                                                                    102;
                                                                                                          h 16.9%;
Similarity 36.0%;
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Similarity 32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S47133
S47133
                                                                                                                                                                                      #8/2: 81/2: 98/1
#superfamily Streptomyces chitinase chi40
glycosidase; hydrolase
#length 424 #molecular-weight 46298 #ch
                                                                                                                                                                                                                                                                                                                                                                                                                                 endochitinase gene expressed during mycoparasitism S47133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, June 1994 Characterization of ech-42, a Trichoderma harzianum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S47133 #type complete chittinase (EC 3.2.1.14) - fungus (Trichoderma harzianum) #formal_name Trichoderma harzianum 23-Nov-1994 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carsolio, C.; Gutierrez, A.; Jimenez, Herrera-Estrella, A.
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                                                                              Conservative
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#domain carboxyl-terminal propeptide #status
experimental #label PRO
gth 378 #molecular-weight 42019 #checksum 6689
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#product chitinase/lysozyme PZ #status predicted
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87; M
                                                                           Score 582; DB 5;
Pred. No. 2.42e-82;
69; Mismatches 95
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Pred. No. 1.33e-84;
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FEATURE
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35-423
SUMMARY
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##cross-references GB:X64104
This enzyme is essential
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                                                                                                                                       kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv 287
                                                                                                                                                                                     GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA 201
                                                                                                                                                                                                   -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-1g 228
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VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                           gcysydpstkelisfdtpamistkvswlkgkglggsmfw
                                                                             lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak 339
                                                                                                                       QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
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                                                           LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                                                                                                                                                                                                                                                101;
                                                                                                                                                                                                                                                                                                            h 16.7%;
Similarity 36.2%;
101; Conservative
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JQ1975
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03-Feb-1994 #sequence_revision 0:
03-May-1996
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#product chitinase 1 #status predicted #label MAY
#length 423 #molecular-weight 46072 #checksum 8802
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Gene (1992) 120:243-248
Primary structure of a chitinase-encoding gene (chil) from
the filamentous fungus Aphanocladium album: Similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial chitinases
                                                                                                                                                                                                                                                                                                            Score 576; DB 5; Length 423; Pred. No. 3.26e-81; 65; Mismatches 95; Indels
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##molecule_type DNA
##residues 1-423 ##label GAR
SUMMARY #length 423 #molecular-weight 46056 #checksum 2000
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.3%; Score 561; DB 12; Length 423; Best Local Similarity 35.7%; Pred. No. 2.14e-78; Matches 101; Conservative 71; Mismatches 94; Indels 17; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #accession
                                                                 111 qlfk-vkkanrglkvllsiggwtwst-nfpsaastdanrknfaktaitfmkdwgfdgidi 168
                                                                                                                                                                                                                                                                  138 DWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEV 197
                                                                                                                                                                                                                                                                                       169 dweyp-adatqasnmilllkevrsqrdayaaqy-apg-yhflltiaapagkdny-sklrl 224
                                                                                                                                                                                                                                                                                                                                        78 QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia, I.; Lora, J.M.; de la Cruz, J.; Benitez, T.; Llobell, A.; Pintor-Toro, J.A.
Curr. Genet. (1994) 27:83-89
Cloning and characterization of a chitinase (CHIT42) cDNA from the mycoparasitic fungus Trichoderma harzianum.
S51369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S51369 #type complete
chitinase - fungus (Trichoderma harzianum)
#formal_name Trichoderma harzianum
15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change
03-May-1996
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 27 16:46:47 1997; MasPar time 14.60 Seconds 676.776 Million cell updates/sec

Tabular output not generated.

Title: >US-08-663-618A-2 (1-466) from US08663618A.pep

Description: Perfect Score: Sequence:

1 MVRSVAWAGEMVLLMIPWGS.....QQSCPTGLVFSNSCKCCTWN 466

PAM 150 Gap 11

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries Searched: 59021 seqs, 21210388 residues

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 50.012; Variance 83.709; scale 0.597

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
1519 1086 1091 698 576 576 5461 437 337 337 263 317 287 172 172 172 172 172 172 172 172 172 17	Score
34.1 29.5 29.5 29.5 20.3 116.3 115.3 115.3 9.8 8.3 7.6 8.3 3.2 5.0 3.2 5.0 3.3 3.3 3.3	Query Match
383 504 699 423 423 427 563 563 561 610 610 611 610 617 617 617 617 617 617 617 617 617 617	Length
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CARTILAGE GLYCOPROTEI ENDOCHITINASE PRECURS ENDOCHITINASE PRECURSOR CHITINASE A1 PRECURSOR 42 KD ENDOCHITINASE 1 PRECURSOR PROCHITINASE 1 PRECURSOR PROBABLE ENDOCHITINASE CHITINASE A PRECURSOR CARTILAGE GLYCOPROTEI ESTRADIOL-DEPENDENT OHYPOTHETICAL 55.6 KD EXOCHTINASE 1 PRECURSOR COPROPORPHYRINOGEN IUMUC PROTEIN.	Description
0.00e+00 2.83e-227 1.18e-213 3.91e-132 7.50e-103 7.50e-60 1.2e-96 9.12e-96 1.2e-60 2.40e-47 1.46e-47 1.45e-39 1.37e-36 1.89e-31 4.12e-13 8.28e-10 1.57e-04 1.57e-04 1.57e-04 1.57e-04 1.57e-04 1.57e-04	Pred. No.

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VIRB4 PROTEIN PRECURS PUTATIVE FAMILY 31 GL	GTP CYCLOHYDROLASE II MOLYBDOPTERIN BIOSYNT		VASCULAR ENDOTHELIAL	EXTRACELLULAR SERINE	, TYPE II	TYPE II	H	TYPE II	KERATIN, TYPE II CYTO	SOLUBLE EPOXIDE HYDRO	SOLUBLE EPOXIDE HYDRO	PUTATIVE PROTEIN DISU	LYSYL-TRNA SYNTHETASE	PUTATIVE PEPTIDASE IN	HOMEOBOX PROTEIN MSX-	ALPHA-GLUCOSIDASE PRE	EXTRACELLULAR SERINE	GLUCOAMYLASE 1 PRECUR	EXOTOXIN TYPE B PRECU	HYPOTHETICAL 40.9 KD
2.71e+00 2.71e+00	2.71e+00 2.71e+00	2.00e+00	2.00e+00	7.97e-01	2.00e+00	2.00e+00	1.09e+00			2.00e+00	1.48e+00	2.00e+00	7.97e-01	2.00e+00	1.48e+00	3.09e-01	3.09e-01		5.83e-01	4.25e-01

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01-DEC-1992 (REL. 2
01-FEB-1995 (REL. 3
01-FEB-1995 (REL. 3
ENDOCHITINASE PRECU
BRUGIA MALAYI.
                                                                                                                                                                 CHAIN
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DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                          REPEAT;
SIGNAL
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PROC. NATL. ACAD. SCI. U.S.A. 89:1548-1552(1992).
-!- FUNCTION: THE MF1 ANTIGEN IS A MICROFILARIAL CHITINASE,
FUNCTION TO DEGRADE CHITIN-CONTAINING STRUCTURES IN THE
FILARIA OR IN ITS MOSQUITO VECTOR DURING PARASITE DEVELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MEDLINE; 92179220.
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    26
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DEVELOPMENTAL STAGE: THE APPEARANCE OF THE MF1 ANTIGEN CORRESPOND MITH THE ONSET OF THE PARASITE'S ABILITY TO INFECT THE MOSQUITO. SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                 L; M73689; G1560
; A38221; A38221
SITE; PS01095; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-ACETYL-D-GLUCOSAMINE PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMISSION.
CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                             GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                         GLYCOSIDASE; CHITIN DEGRADATION; YCOPROTEIN; CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAZOA; ACOELOMATES;
                                                                                31.5%;
larity 42.8%;
Conservative
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400
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148
15971
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24, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDAT
CURSOR (EC 3.2.1.14) (MF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLYSIS
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                                                                                                                                                                 MW.
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                                                                                                                                                             ENDOCHITINASE.

CATALYTIC.

SER/THR-RICH (LINKER).

3 X 14 AA APPROXIMATE TANDEM RE
PROTON DONOR (BY SIMILARITY).

W; 4DA7E5EB CRC32;
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Pred.
94; M
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. No. 2.8
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S OF CHITIN.
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2.83e-227;
ches 102;
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                                                                                                                      Length
                                                                                                                                                                                                     TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKAGES
                                                                                                                                                                                                                                                                                                                                ANTIGEN
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                             Query Match
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CARBOHYD
CARBOHYD
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01-JUN-1994 (REL. 29, LAST SEQUENCE UP
01-FEB-1995 (REL. 31, LAST ANNOTATION
ENDOCHITINASE PRECURSOR (EC 3 2 1.14).
MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBA
EUKARYOTA; METAZOA; ARTHROPODA; INSECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHIT_MANSE
P36362;
                                                                                                                                                                            EMBL; U02270; G406049;
EMBL; S64757; -; NOT_AI
HSSP; P07254; ICTN.
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                                                                                                                                                                                                                                                                                                                               KRAMER K.J., CORPUZ L., CHOI H.K., MUTHUKRISHNAN INSECT BIOCHEM. MOL. BIOL. 23:691-701(1993).
-!- FUNCTION: DIGEST CHITIN IN THE EXOSKELETON DU
                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
DYVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH HINSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A RAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LC LEVELS SEEN ON DAYS 0, 7 AND 8.
TISSUE SPECIFICITY: EPIDERMIS AND GUT.
                                                                                                                                                                                                                     SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                             HYDROLASES)
avtklretnpglkvllsyggynfgsaiftgiaksagkterfiksaiaflrknnfdgfdld
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRI
                                       Similarity
                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
93357793.
                                                                                                                                                                      PS01095;
                                                                                                                                                  GLYCOSIDASE;
                                                                     396
146
146
303
407
554
                             29.9%;
larity 38.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).
TAZOA; ARTHROPODA; INSECTA; LEPIDOPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                               554
453
146
85
85
303
307
545
545
52203
                                                                                                                                                                                        NOT_ANNOTATED_CDS
                                                                                                                                                          CHITINASE_18.
IDASE; CHITIN DEGRADATION;
                                                                                                                                                                                                                      ö
                                                                    MW;
                                                                                                                                                                                                                                SECRETED
                             Score
Pred.
105; M
                                                                                                                                                                                                                      CHITINASE
                                                                   PROTON DONOR
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
FAB7FBAD CR
                                                                                                                              ENDOCHITINASE
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                              Mismatches
                                       1031;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 UPDATE
                                                                                                                                                                                                                      CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              554
                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
                             DB 2; I
.18e-213;
ches 126;
                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                           LEPIDOPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                      (BY
                                                                                                                                                                                                                     II
                                                                                                                                                            SIGNAL; GLYCOPROTEIN
                                                                                                                                                                                                                     (FAMILY
                                                                                                                                                                                                                                                                                                                               DURING
                                                Length
                              Indels
                                                                                                                                                                                                                                                                                                                               HE
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                                                                                                                                                                                                                                                                                                                               MOLTING
                              25;
                             Gaps
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THE THE TENT OF TH
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  Query Match
Best Local
                                                        ACT_SITE
MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHI1_BACCI
P20533;
                                                                                                                                                                                                                                                                                                                                                                      J. BIOL. CHEM. 268:18567-18572(1993).

-I- CAPALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GL
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WL-12;
MEDLINE; 93365760.
WATANABE T., KOHORI K., MIYASHITA K.,
UCHIDA M., TANAKA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WL-12;
MEDLINE; 90368776.
                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATANABE T., SUZUKI K., OYANAGI W., (
J. BIOL. CHEM. 265:15659-15665(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACILLUS CIRCULANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHITINASE A1
                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                                                                                                        HYDROLASES).
                                                                                                                                                                                                                                                                                             A38368; A38368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dvdkngfrnftsIrsshpsvkfmvavggwaegsskyshmvaqkstrmsfirsvvsflkky
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDLDDFAGFSCNQGRYPLIQTLRQELSLPY-LPSGTPELEVPKPGQPSEPEHGPSPGQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVCS--WKG-A--TKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QWLQKGTPASKLILGMPTYGRSFTLASSSDT-RVGA--P-ATGSGTPGPFTKEGGMLAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-DETLYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPWGSAAKLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTN-H-Q-LST-TEW
                                                                                                                                                                                                                                                                                                                                  M57601;
  Similarity
                                                                                                                                                                                                                                                                           07254; 1CTN; PS01095; (
                                                                                                                                                                                                                                                       GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 17, C. (REL. 17, L. ) (REL. 31, L. ) (REL. 31, L. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                    G142688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                699
460
549
544
204
200
200
200
200
73677
                                                                                                                                                                                                                                                     CHITINASE_18.
IDASE; CHITIN
  20.3%;
40.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENT ANNOTATION (EC 3.2)
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                                                            ¥Ε
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ANNOTATION
3.2.1.14).
                                                                        CATALYTIC.
FIBRONECTIN TYPE-III (R-1).
FIBRONECTIN TYPE-III (R-2).
FIBRONECTIN TYPE-III (R-2).
PROTON DONOR (PROBABLE).
D-N: DECREASE IN ACTIVITY.
D-YE: NO CHANGE IN ACTIVITY.
E->D,Q: LOSS OF ACTIVITY.
Score 698; DB 2; I
Pred. No. 3.91e-132;
                                                                                                                                                                                                                CHITINASE A1.
                                                        ->D,Q: LOS
5A1777CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                     DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OHNISHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUJII T.,
                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RODS
                                                                                                                                                                                                                                                                                                                                                                          II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...
:
                                                                                                                                                                                                                                                     SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCCI;
                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ε:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
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                                                                                               Matches
                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                          EMBL; X64104; G42902b; -.
PIR; JQ1975; JQ1975.
HSSP; P07254; 1CTN.
PROSITE; PS01095; CHITINASE_18.
PROSITE; PS01095; CHITINASE_18.
PROSITE; PS01095; CHITINASE_18.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993
01-FEB-1996
01-FEB-1996
                                                                                                                                    CHAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                MEDLINE: 92136437.
BLAISEAU P.-L., KUNZ C., GRISON R., CURR. GENET. 21:61-66(1992).
                                                                                                                                                                                                                                                                                                                                MEDLINE; 93013040.
BLAISEAU P.-L., LAFAY J
GENE 120:243-248(1992).
                                                                                                                                                                                                                                                                                                    SEQUENCE OF 35-57
MEDLINE; 92136437
                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                             STRAIN-ETHM 483
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                  APHANOCLADIUM ALBUM
                                                                                                                                                                                                                                                                                                                                                                                                                     CHITINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P32470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHI1_APHAL
                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: HYDROLYSIS
                     143
                                                                      115 lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 173
  229
                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379
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                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                   HYDROLASES)
                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO CHITINASE CLASS
                                                                                                                                                                                                                                                            N-ACETYL-D-GLUCOSAMINE POLYMERS
kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv
                             W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL
                   GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                         LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hldagvpaaklvlgvpfygrgwd-gcaqagn-ggyqtctggssvgtweagsfdfydlean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ntelakiaaivdwinimtydfngawqkisahnaplnydpaasaagvpdantfnvaagagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEV-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPL-YKRQE-ESGAA-A-SLNVDAAVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEYP--GS-QG-S-PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD
                                                                                               101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119;
                                                                                                        Similarity
                                                                                                               FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                  (REL. 27, CREATED)
(REL. 33, LAST SEQUENCE UP
(REL. 33, LAST ANNOTATION
PRECURSOR (EC 3.2.1.14).
                                                                                             16.7%;
llarity 36.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         DEUTEROMYCOTINA
                                                                                                                                                                                                                                                                                                                                          J.-F.;
                                                                                                                                                                                                                                                      SECRETED
                                                                                             Pred.
                                                                                                       Score 576;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                              CHITINASE 1. PROTON DONOR
                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                    88456E6E
                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         (IMPERFECT FUNGI).
                                                                                                                                                                                                                                                                       OF THE
                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                           BERTHEAU
                                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423
                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
                                                                                                        DB 2; I
                                                                                                                                    CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                              (BY
                                                                                                                                                                                                                                                                       BETA-1,4
                                                                                                                                                                                                                                           H
                                                                                                                                                                                   SIGNAL;
                                                                                                                                                                                                                                                                                           Υ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                           (FAMILY
                                                                                                                Length
                                                                                                                                                                                                                                                                                           BRYGOO
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                       LINKAGES
                                                                                                                                                                                   ZYMOGEN
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                                                                                             18;
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                                                                                                                                                                                                                                                                       ဓ္ဗ
                                                                                                                                                                                                                                            GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
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Best Local S
Matches 10
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SIGNAL 1
PROPEP 23
CHAIN 35
ACT_SITE 171
CARBOHYD 218
SEQUENCE 423 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHI4_TRIHA
P48827;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENT:
- CATALYTIC ACTIVITY: HYDROLYSIS OF ACTIVIDATION POLYMERS OF SUBCELLULAR LOCATION: SECRETED.
- INDUCTION: SPECIFICALLY INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PINTOR TORO J.A.;
PINTOR TORO J.A.;
CURR. GENET. 27:83-89(1994).
-I- FUNCTION: MORPHOGENETIC ROLE DURING APICAL GROWTH, CELL DIV.
-I- FUNCTION: MORPHOGENETIC ROLE DURING APICAL GROWTH, CELL DIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S78423;
HYDROLASE; GL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND MEDLINE; 95269313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRICHODERMA HARZIANUM.
EUKARYOTA; FUNGI; DEUTEROMYCOTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
42 KD ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS
  318
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                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLASES)
                        nkivlgmpiygrsf--qntag--igqtyngvgs-gsw--eagiwdykalpk-agatvqyd
                                                                                                                                                                            adlgqvldyinlmaydyagsfspltghdanlfnnpsnpnatp-fntdsavkdyinggvpa
                                                                                                                                                                                                                                   QDQKVPYIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                       DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
                                                                                                                                                                                                                                                                                                                 QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                             SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRI
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                                                                                                                                                                                                                                                                                                                                                                                                                  16.3%;
Similarity 35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LORA J.M., LA CRUZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 P
34 4
423 4
171 P
218 P
46056 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 KD ENDOCHITINASE
PROTON DONOR (BY S:
POTENTIAL.
PW; 899DA50A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHITINASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                             Score 561; DB 2;
Pred. No. 2.55e-99;
71; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               17;
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Best Local Similarity 34.1%;
Matches 95; Conservative
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P54196;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENDOCHTINASE I PRECURSOR (EC 3.2.1.14) (COMPLEMENT-FIXATION CP-ANTIGEN) (CF-AG).
                  CHIA_SERMA
P07254;
01-APR-1988
01-FEB-1995
01-FEB-1995
CHITINASE A
CHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
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CARBOHYD
CONFLICT
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SUBMITTED (MAR-1996) TO EMBL/GENBANK/DEBU DATA BANKS.
SUBMITTED (TOTAL TUTTY HUDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N. STRAIN-SILVEIRA; YANG C., ZHU Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96144270.
PISHKO E.J., KIRKLAND T
GENE 167:173-177(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L41663; G1200190;
EMBL; U51271; G1256769;
EMBL; U33265; G1255728;
HYDROLASE; GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C735
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                                                                                                                                                                                                                                             322
                                                                                                                                                                                                                                                                                         340
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                                                                                                                                                                                                                                                                                                                              ede-kqandfvlllkacrealdaysak-hpngk-kflltiaspagpqny-nk-lklaemd 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lkknnrnlktllsiggwty-spnfktpasteegrkkfadtslklmkdlgfdgididweyp 173
                                                                                                                                                                                                                                           VPYIF-RDNOW-VGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                                                                                asysydknkrylisydtvkiagkkaeyitkngmgggm-w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA 201
                                                                                                                                                                                                                                                                                                                                                                                                                      QNLDFYNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 142
                                         (REL. 07, 6 (REL. 31, 5 (REL. 31, PRECURSOR
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427 i
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                                                                                                                                                      STANDARD;
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427
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                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
(EC 3.2.1.14).
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Pred. No. 9.12e-96;
71; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMSSMPNYYPVPEAPEGGFRSVVYFVNW
K -> N (IN REF. 2).
; 6CB9AF73 CRC32;
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POTENTIAL.
RWLSLRCLFCELGRFMFTLSTVTAVTVVTDDIQ
                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                             358
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
PERRAKIS
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
JONES J.D.G., GRADY K.L.,
EMBO J. 5:467-473(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; GRACILICUTES; ENTEROBACTERIACEAE.
                                                                                                              349
                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                            HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                    PIR; A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VORGIAS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS, AND X-RAY CRYSTALLOGRAPHY MEDLINE; 95219379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. KOO J.C., LIM C.O.,
342
                                                464
                                                                              406
                                                                                               169
                                                                                                                               115
                                                                                                                                              290
                                                                                                                                                                        287
                                                               227
                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                           ; L01455; G152818; -.; X03657; G46831; -.
A25090; A25090.
; P07254; LCIN.
                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASES)
                                                             TKVSYLKQKGLGGAMVWALDLDD
               akgkyvldkqlgglfsweidadn
                                        lsaetgr-kyeltsaisagkdkidkvaynvaq--nsmdhiflmsydfygpfdlknlghqt
: :|::|::|::| :| :|:|
EAQTSGKERLLLSAAVPAGQTYYD-AGYEVDKIAQNLDFYNLMAYDFHGSWE-KYTGHNS
                                                                                                                                           -rdrfvgsvkeflqtwkffdgvd1dwefpggkganpnlgspqdgetyvl1mkelramldq
                                                                                                                                                            AFAGMTNHQLSTTEWNDE-T-LYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATAN
                                GSGTPGPFTKEGGMLAYYEVCS-WKGATKQ-RIQD-QKVPYIFR-
                                                                                                                                                                                             Similarity
93; Conse
                                                                                                                                                                                                                                                                                                                                                                    PS01095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A., TEWS I., DAUTER Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JAN-1993)
                                                                                                                                                                                                                                                                                                                                                            GLYCOSIDASE;
                                                                                                                                                                                            12.7%;
larity 28.8%;
Conservative
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IDASE; CHITIN
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467
473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSLOW
                                                                                                                                                                                                                                                  A -> P (IN REF. 2).
V -> I (IN REF. 2).
P -> A (IN REF. 1 AND 2)
PAWKPDTAYTTYNGVWALLAQ ->
PAWKPDTAYTTYNGVWALLAQ ->
AAGQ (IN REF. 1 AND 2).
V -> I (IN REF. 2).
ATGP -> HRA (IN REF. 2).
                                                                                                                                                                                                    Score 437; DB 2;
Pred. No. 2.88e-70
                545
                                                                                                                                                                                                                                  ATGP
                                                                                                                                                                                                                                                                                                                           CHITINASE A. CATALYTIC. PROTON DONOR
364
                                                                                                                                                                                                                                                                                                           PROBABLE.
TA -> GP (IN REF
                                                                                                                                                                                                                           -> E (IN REF. 2).
-> S (IN REF. 2).
7764DB57 CRC32;
                                                                                                                                                                                                                                                                                                                                                            DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIM C.Y.,
                                                                                                                                                                                             Mismatches
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                                                                                                                             -DKERFTTLVQDLANAFQQ
                                                                                                                                                                                                           Length
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Best Local S
Matches S
                                                                                     CHIA_ALTSO
P32823;
01-OCT-1993
01-OCT-1993
01-FEB-1995
CHITINASE A
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P41684;
01-NOV-1995
01-NOV-1995
01-NOV-1995
PROBABLE END
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
ACT_SITE
CARBOHYD
VIBRONACEAE [1]
                                    ALTEROMONAS PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYRES M.D., HOWARD S.C., KUZIO J., LOPEZ-FERBE VIROLOGY 202:586-605(1994).
-:- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
02-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
03-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-N
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PROSITE; PS01095; CHITINASE_18
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ANNRQTEVNSAIRELRKYSE-DGLDLDWEYPGSQGS-PAV-D-K-E-R-FTTLVQDLANA
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                                                                                                                                                                                                                                                                                                                              APATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQ-KVPYIF-RDN-QWVGFDDVES
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95; Conser
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(REL. 27,
(REL. 31,
PRECURSOR
                                  SP. (STRAIN O GRACILICUTES;
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                                                                                                                                                                                  STANDARD;
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305
173
444
551
61368
                                                                                   27, CREATED)
27, LAST SEQUENTS ANNOTED SEQUENTS ANNOTED SEQUENCES 3.2.
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                                                                                     r SEQUENCE UPDATE) r ANNOTATION UPDATE) 3.2.1.14) (CHI-A).
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                                    SCOTOBACTERIA;
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Pred.
80; M
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1. No. 1.25e-60;
1. no. 1.25e-61;
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                                    FACULTATIVELY ANAEROBIC
                                                                                                                                                                                B
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EUBACULOVIRINAE.
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TRESULTATION OF THE MAN SET OF THE M
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Best Local S
Matches 5
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P11797;
01-OCT-1989
01-OCT-1989
01-FEB-1995
CHITINASE B
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ACT_SITE
SEQUENCE
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TSUJIBO H
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J. BACTERIOL.
                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 990 / OMB1466;
MEDLINE; 99845110.
HARPSTER M.H., DUNSMUIR P.;
NUCLEIC ACIDS RES. 17:5395-5395(1989).
-I- CATALYTIC ACTIVITY: HDROLYSIS OF THE BETA-1,4 LINKAGES
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 L)
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-I- ENZYME REGULATION: STIMULATED BY MG2+; INHIBITED
N-BROMOSUCCINIMIDE AND 2-HYDROXY-5-NITROBERNYL BE
-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMIL)
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MEDLINE; 93106952.
TSUJIBO H., ORIKOSHI H., TANNO H
IMADA C., OKAMI Y., INAMORI Y.;
J. BACTERIOL. 175:176-181(1993).
  PIR;
                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                   SERRATIA MARCESCENS.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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                                                          HYDROLASES)
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P07254; LCTN.
PS01095; CHITINASE_18.
PS01095; CHITIN DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBO H., YOSHIDA Y., MIYAMOTO K.,
J. MICROBIOL. 38:891-897(1992).
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                             X15208;
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22
313
820
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(REL. 12, LAST SEQUENCE UP
(REL. 31, LAST ANNOTATION
PRECURSOR (EC 3.2.1.14).
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87346 MW;
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Pred. No. 2.
44; Mismatc
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PROTON DONOR
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RATURE OF CHI-A ARE
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CRC32;
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Matches 5
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SIGNAL
CHAIN
ACT_SITE
SEQUENCE
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FUJII T., MIYASHITA K.;
J. GEN. MICROBIOL. 139:677-686(1993).
J. CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES
-!- CATALYTIC ACTIVICOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                   DOMAIN
ACT_SITE
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                                                                                                                                                                                                                                                                        HYDROLASE;
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P36909;
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01-FEB-1995
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                  WNDETLYQEFNGLKKMN----PKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFL 127
                                                                                                                                                                                                                                                                                                                                                                                                                       D12647;
P07254;
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PS00561; CBD_BACTERIAL.
PS01095; CHITINASE_18.
PS01095; CHITIN DEGRADATION;
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GLYCOSIDASE; CHITIN DEGRADATION;
1 41
1 42
42 499
144 144
499 AA; 55464 MW; 9A585FFC CRC:
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(REL. 29,
(REL. 31,
PRECURSOR
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llarity 28.2%;
Conservative
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larity 34.0%;
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, LAST SEQUENCE UPI
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R (EC 3.2.1.14).
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                                                                                                                                                                                                                                                                        CELLULOSE-BINDING.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                CHITINASE
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No. 1
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No. 1.46e-47;
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L.25e-39;
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                                                                         Query Match
Best Local S
Matches 7
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EMBL; M18397; G153209; -.
PIR; A29912; A29912.
PIR; JH0573; JH0573;
HSSP; P07254; 1CTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIT_STRPL STANDARD; PRT; 6: p11220; 01-JUL-1989 (REL. 11, CREATED) 01-DEC-1992 (REL. 24, LAST SEQUENCE UP) 01-FEB-1995 (REL. 31, LAST ANNOTATION CHITINASE 63 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                   ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                           DOMAIN
DOMAIN
ACT_SIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROBBINS P.W., ALBRIGHT C., BENFIELD B.;
J. BIOL. CHEM. 263:443-447(1988).
I- CATALYTIC ACTIVITY: HYDROLYSIS OF T
N-ACETYL-D-GLUCOSAMINE POLYMERS OF
I-INDUCTION: BY CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del> - <del>-</del> -
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MEDLINE; 92192480.
ROBBINS P.W., OVERBYE K.,
GENE 111:69-76(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOMYCES
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                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                     320
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                               fnqlrnlkaeyphikilysfggwtwsgg-fpdavknpaafakschdlvedprwadvfdgi
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                                                                         h 8.3%;
Similarity 26.4%;
78; Conservative
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PS00561; CBD_BACTERIAL.
PS01095; CHITINASE_18.
PS01095; CHITINASE_17.
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                                                                         Score 287;
Pred. No. 1.
63; Mismatc
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                                                                                                                                                                                                             CHITINASE 63.
CELLULOSE-BINDING.
FIBRONECTIN TYPE-III.
CATALYTIC.
                                                                                                                                                                       PROTON DONOR (BY SIMILARITY).
F -> I (IN REF. 2).
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                                                                                             DB 2; 37e-36;
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                                                                           134;
                                                                                                                                                                                                                                                                                                             CHITIN-BINDING;
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                                                                         Gaps
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                          -!- SIMILARITY: LOCAL, TO
-!- SIMILARITY: BELONGS T
EMBL; X01127; G2829; -.
EMBL; X00762; G2844; -.
EMBL; X01095; G2849; -.
PIR; S07915; S07915.
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 85037931. TOKUNAGA M., KAWAMU NUCLEIC ACIDS RES.
                                                                                                                                                                                                                                                                                                                                                                             CHITINASE ACTIVITY OF ALPHA-SUBUNIT.
MEDLINE; 91301161.
BUTLER A.R., O'DONNEL R.W., MARTIN V.J., GOODAY G.W.,
EUR. J. BICCHEM. 199:483-488(1991).
-i- FUNCTION: THE ALPHA SUBUNIT IS A POTENT EXOCHITINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
KILLER TOXIN ALPHA AND BETA SUBUNITS PRECURSOR
(ENDOCHITINASE (EC 3.2.1.14)).
KLUYVEROMYCES LACTIS (YEAST).
                                                                                                                                                                                                                      TOXIN WITH SENSITIVE CELLS AND ALLOW THE GAMMA SUBUNIT TOXIN) TO GAIN ENTRY INTO THE CELL.

-i- PTM: RF2 IS POTENTIALLY SPLIT BY MEMBRANE-BOUND BASIC F SPECIFIC ERPTIDASE TO YIELD THE ALPHA AND BETA SUBUNITS OF THREE SUBUNITS THE KILLER TOXIN IS COMPOSED OF THREE SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90259069.
BRADSHAW H.D. JR.;
NATURE 345:299-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION OF PROTEIN, MEDLINE; 87004569.
STARK M.J.R., BOYD A.;
EMBO J. 5:1995-2002(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŚEQUENCE FROM N.A.
MEDLINE; 84297209.
STARK M.J.R., MILEHAM A.J., ROMANOS M.A.,
NUCLEIC ACIDS RES. 12:6011-6030(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P09805;
01-MAR-1989
  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CBS 2359/152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F., FUKUHARA H.;
R. GENET. 9:147-155(1985).
                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THE ALPHA SUBUNIT IS A POTENT EXOCHITINASE. ALONG THE BETA SUBUNIT IT PLAYS A ROLE IN THE INITIAL INTERACTION
                                                                                                                                                                                              BETA AND GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skgvpadklligigfygrgwt-gvtqsap-ggtatgpaa-gty--eagiedy-kvlknsc 545
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PS00026; CHITIN_BINDING
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S.RES. 12:7581-7597(1984).
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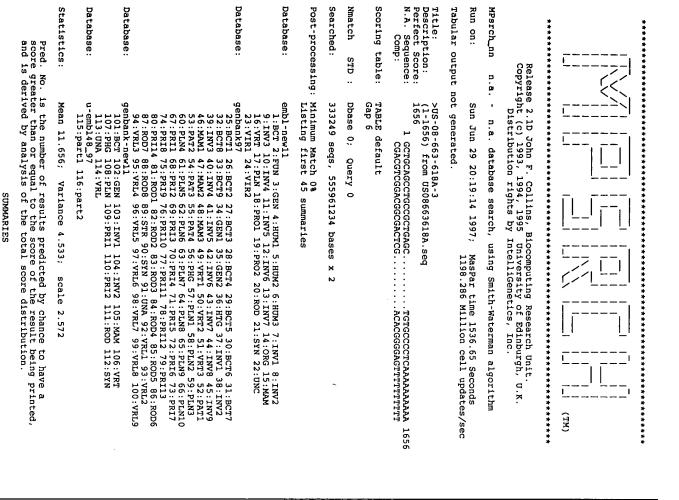
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PIPER CAPACITY OF THE CAPACITY OF RESPOND TO AND COPE WITH CHANGES IN THEIR ENVIRONMENT.
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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CARTILAGE GLYCOPROTEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGME BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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SIMILARITY: BELONGS TO FAMILY 18 OF (
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TISSUE SPECIFICITY: MAMMARY SECRETIONS
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TOXIN; GLYCOPROTEIN; S
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OTEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGMENT).
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11; Mismatches 7;
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58; Mismatches 74
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ALIGNMENTS

	JOURNAL	TITLE	AUTHORS	REFERENCE	MEDLINE	JOURNAL		TITLE		AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	RESULT 1
AMC, E.C. Slater, Institute, University of Amsterdam, Meibergdreef 15, 1105 AZ, Amsterdam, The Netherlands	Submitted (21-JUN-1995) Rolf G. Boot, Department of Biochemistry,	Direct Submission	Boot, R.G.	2 (bases 1 to 1633)	96064695	J. Biol. Chem. 270 (44), 26252-26256 (1995)	produced by macrophages	Cloning of a cDNA encoding chitotriosidase, a human chitinase	Aerts, J.M.	Boot, R.G., Renkema, G.H., Strijland, A., van Zonneveld, A.J. and	1 (bases 1 to 1633)	Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	Homo sapiens	human.		91050957	U29615	Human chitotriosidase precursor mRNA, complete cds.	HSU29615 1633 bp mRNA PRI 04-NOV-1995	

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                                         cttgactgggagtacccaggaagccagggagccctgccgtagacaaggagcgcttcaca
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EKYTGHNSPLYKRQEESGAAASINYDAAVQQWLQKGTFASKLILGMPTYGRSFTLASS
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/clone_lib="macrophage-1 cl
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Human cartilage gp-39, a major secretory product chondrocytes and synovial cells, is a mammalian nuchitinase protein family
J. Biol. Chem. 268 (34), 25803-25810 (1993)
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/cell_type="chondrocyte"
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                     Vertebrata; Eucheria; Primates; Catarrhini; Hominida 1 (bases 1 to 1418)
Hu.B., Trinh,K., Figueira,W.F. and Price,P.A.
Isolation and sequence of a novel human chondrocyte to mammalian members of the chitinase protein family J. Biol. Chem. 271 (32), 19415-19420 (1996) 96325055
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Human YKL-39
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TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	TITLE	TITLE JOURNAL REFERENCE AUTHORS	AUTHORS			RESULT 4 LOCUS DEFINITION	Qy 1115 TG	Db 1115 tg	Db 1055 gg 1 Qy 1055 GG	Db 995 ct. Oy 995 CT	Db 935 tg. Qy 938 TG	Qy 878 AG	818 818	758 758	698	Db 698 ca	Db 638 ca Qy 644 TG	578 584
Direct Submission Submitted (17-MAY-1996) Medical Biophysics, Ontario Cancer Institute, Princess Margaret Hospital, 610 University Avenue, Toronto, Ontario M5G 2M9, Canada	Unpublished 3 (bases 1 to 1434) Grossman, A., Matsuyama, T., Baker, E., Waterhouse, P., Sutherland, G.R. and Mak T.	and Mak, T. W. Choning of a novel lymphoid restricted human chitinase and localization to 1513 2	The WashU-Merck EST Project Unpublished 2 (bases 1 to 1434) 6 (bases 1 to 1434) 6 (bases 1 to 1434)	Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.	Nomo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (hases 1 to 1434)	58514 1439565 uman.	HSU58514 1434 bp mRNA PRI 24-JUL-1996 Human chitinase precursor (HUMTCHIT) mRNA, exon la form, complete	TGACTTTGCCGCTTCTCCTGCAACCAGGGCCGATACCCCCTCATCCA 1162	acttcactggcaaatcctgcaaccagggcccttaccctcttgtcca 1162	ggttcagttcttaaagaatttaaacctgggaggagccatgatctggtctattgacatgga 1114 	ctacgcagtcaaggggaaccagtgggtgggctatgatgatgtgaagagtatggagaccaa 1054 	tgagatctgccagttcctgaaaggagccaagatcacgcgcctccaggatcagcaggttcc 994 	Tgcctctggccttggagctgctggacccatcacagagtcttcaggcttcctggcctatta 934		atatgctgtggggtactggatacataagggaatgccatcagagaaggtggtcatgggcat 817 TGCTGCTGTCAACAGTGGCTGCAGAAGGGGACCCCTGCCAGCAAGCTGATCCTTGGCAT 817		aacagccctctgagcaaggggtggcaggacagagggccaagctcctactacaatgtgga 757	catcaacctcctgtcctttgacttccatgggtcttgggaaaagccccttatcactggcca 697	agggaggcaaatgattgataacagctatcaagttgagaaactggcaaaagatctggattt 637

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Vertebrata;
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rtebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1500)
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                                                                                                                                                                                                                                                                 /evidence=not_experimental
/gene="HUMYCHIT"
/note="submitter can find no appropriate Kozak initiator
/note="submitter can find penomic frame continuing
/note="submitter can find genomic sequencing; use of a Met
further downstream as the initiator Met would result in
the deletion of amino acids conserved in all other family
members; submitter hypothesizes that an Ile is the
initiator codon for this form; second alternatively
spliced form; see GenBank Accession Number U58514 for the
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/gene="HUMTCHIT"
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                                                                              Direct Submission

Submitted (19-JAN-1995) Millis A. J., University at Albany,
Biological Sciences, 1400 Washington Avenue, Albany, NY, USA, 12222

(bases 1 to 1733)

Shackelton, L. M., Mann, D. M. and Millis, A. J.

Identification of a 38-kDa heparin-binding glycoprotein (gp38k) in
differentiating vascular smooth muscle cells as a member of a group
of proteins associated with tissue remodeling
J. Biol. Chem. 270 (22), 13076-13083 (1995)
                                                                                                                                                                                                                                                       gp38k; heparin-binding
pig
Sus scrofa
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S.scrofa 38kDa heparin-binding
Z47803
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Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Su
1 (bases 1 to 1733)
Millis,A.J.
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          /organism="Sus scr
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/dev_stage="adult"
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Sus scrofa
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Vertebrata;
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Identification of a 38-kDa heparin-binding glycoprotein (gp38k) in differentiating vascular smooth muscle cells as a member of a group of proteins associated with tissue remodeling J._Biol. Chem. 270 (22), 13076-13083 (1995)
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University at Albany, 1400 Wa
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/db_xref="plD:g643471"
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/dev_stage="adult"
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    Albert J.T. Millis, Biological
1400 Washington Avenue, Albany,

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Shackelton L.M., Mann D.M., Millis A.J.;

"Identification of a 38-kba heparin-binding glycoprotein
in differentiating vascular smooth muscle cells as a memb
group of proteins associated with tissue remodeling";
J. Biol. Chem. 270:13076-13083(1995).
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28-AUG-1996 (Rel. 49, Last updated, Version 6)
28-SCTOÍA 38kDa heparin-binding glycoprotein.
gp38k; heparin-binding glycoprotein.
Sus scrofa (domestic pig)
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Theria; Eutheria; Artiodactyla; Suiformes; Suidae.
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                                                                                                                                          GTGGCCTGGGCAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCTGCTGCAAAACTG
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687; Conser
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J., University at Albany, Biological Sciences, 1400
n Avenue, Albany, NY, USA, 12222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                         9.3%;
llarity 62.5%;
Conservative
                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
/clone="pBS38k"
/dev_stage="adult"
/tissue_type="smooth muscle"
/clone_lib="lambda ZAP II"
67. 1218
                                                                                                                                                                                                                                      LKSRQLAGAMVWTLDLDDFRGNFCGQNLRFPLTSAIKDVLAAA"; 408 A; 507 C; 463 G; 355 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                              /product="38 kDa heparin-binding glycoprotein"
/db_xref="PID:g634098"
/translation="MGLRVAQTGFVALVLLQSCAAYKLVCYYTSWSQYREGDGSCFPD
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Pred. No. 1.
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RESULT 9
LOCUS
DEFINITION
ACCESSION

M.musculus X93035 MMBRP39

mRNA

1616 bp RNA for E

p RNA BRP39 pi

protein

ROB

28-NOV-1995

SOURCE ORGANISM

KEYWORDS

g1085065 brp39 gene; B house mouse. Mus musculus

BRP39

protein

Eukaryotae; m Vertebrata; E Murinae; Mus.

mitochondrial eukaryotes; Metazoa; Eutheria; Rodentia; Sciurognathi; 1

; Chordata; Myomorpha;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 8.0%;
l Similarity 62.4%;
673; Conservative
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Submitted (14-NOV-1995) B.W.
Institute, 44 Binney Street,
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/note="leader
66..1211
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//translation="MGMRAALTGERAUMLLQSCSAYKLYCYFTSWSQYREGYGSFLPD
//translation="MGMRAALTGERAUMLLQSCSAYKLYCYFTSWSQYREGYGSFLPD
AIQPFLCTHITYSFANTSDMMLSTWEWNDESNYDKLNKLKTRNTNLKTLLSYGGWKF
GEKRESEIASNTERRTAFYRSVAPFLRSYGFDGLDLAWLYFRLEDKQYFSTLIKELNA
EETKEVQPGREKLLLSAALSQAKVALDTGYDIAQIADHTINLMTYDEHGYWRQITG
HHSPLFQGQKDTRFDRYSNVNYAVQYMIRLGAQASKLLMGIPTFGKSFTLASSENQLG
APISGEGLPGRFTKEAGTLAYYBIDDFLKGAEVHRLSNEKYPFATKGNQWYGYEHKES
APISGEGLPGRFTKEAGTAYYBIDDFLGGTCQFKEFFPLTNAIKDALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="breast"
/cell_line="SMF murine
/clone_lib="lambda ZAP
66...128
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/product="BRP39 protein"
/db_xref="PID:e211795"
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/note="homology to
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/dev_stage="adult"
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"Molecular cloning and eosinophil chemotactic Unpublished.
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Theria; Eutheria; Rodentia;
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Owhashi,M., Arita,H., Taoka,Y. and Hayai,N.
Molecular cloning and characterization of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-SEP-1996) to the DDBJ/EMBL/GenBank databases. Makoto Owhashi, The University of Tokushima, Faculty of Integrated Arts and Sciences; 1-1 Minami-Johsanjima, Tokushima, Tokushima 770, Japan (E-mail:chashi@ias.tokushima-u.ac.jp, Tel:0886-56-7261, Fax:0886-56-7298)
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 ACCAAGGTCAGCTATCTGAAGCAGAAGGGACTGGGCGGGGCCATGGTCTGGGCACTGGAC
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larity 57.1%;
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Sus scrofa
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Buhi, W.C., Choi, I., Cleaver, B.D. and Simmen, F.A.
Molecular cloning and characterization of an estrogen-dependent porcine oviductal secretory glycoprotein (POSP)
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VAPTRPTLSFGKLTVAPEGKTESPGEKAMTPVGHPSVTPGDMSVPPVPIQTGDRITPP
RRQAVAPEKMTLPSGKRSD"
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/tissue_type="oviduct"
/dev_stage="adult"
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Bovidae; Caprinae; Ovis.
1 (bases 1 to 1596)
1 (bases 1, J.T., Brownlee, A.G. and Marshall, J.T., Brownlee, A.G. and archaell, J.T., Brownlee, A.G. and Marshall, Marshal
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2 (bases 1 to 1596)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-DEC-1994) James
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IKREHFGGAMVWTLDLDDFRGNFCGTGPEPLVHTLNNLLVNDEFSSTBSFKFWFSTAV
NSSRIGPEMPTMTRDLTTGLGILPLGGEAVATETHRKSATMTTPRGETATPTRTPLS
SGRRTAAPEGKTESPGEKPLTSVGHLAVSPGGIAVGPVHQIGQKVTPPGRKAGVPEK
VTTPSGKMTVTPDGRAETLERRL"
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STFSINBERFVNSVIALLRTHGEPGLDLEFLYPGLRGSPARDRWITVFLLBELLQAFKI
BAQLIMRERLLLSAAVSGDEHVIQKAYDARLLGELDDFISVLSVDHGSBEKYUGHUS
PLFSLPGDPKSSAYAMSYWRQLGVPPBKLLMGLPTYGRTFHLLRASQNBLGAGAVGPA
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/dev_stage="oestrus"
<1..1596</pre>
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/db_xref="PID:g602294"
/translation="LLLVLKHHDGAAHKLVCYFTNWAFSRPGSASILPRDLDPFLCTH
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Pred. No. 9.79e-59;
0; Mismatches 254
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                                                                                                                           Submitted (05-MAR-1991) Randal C. Jaffe, Department of Physiology and Blophysics, University of Illinois College of Medicine, Chicago, IL 60612-7342, USA Location/Qualifiers
                                                                                                                                                                                                                                                       Jaffe,R.C., Arias,E.B., O'Day-Bowman,M.B., Mavrogianis,P.A. and Verhage,H.G. Regional Distribution and Hormonal Control Oviduct Specific Glycoprotein mRNA in the E Biol. Reprod. (1999) In press
                                                                                                                                                                                                                                                                                                                                                                                     Cloning of a recombinant complementary DNA to a baboon (Papio anubis) estradiol-dependent oviduct-specific glycoprotein Mol. Endocrinol. 5 (3), 356-364 (1991)
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Vertebrata; Eutheria; Primates;
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1 (bases 1 to 2228)
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hamadryas anubis estradiol-dependent
protein mRNA, partial cds.
glycoprotein"
/db_xref="PID:g1256951"
                                                                        /organism="Papio hamadryas
13..1884
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/product="estradiol-dependent oviduct-specific
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Eutheria; Primates; Catarrhini; Cercopithecidae;
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/translation="mwkillwygivivikhhdgaankivorftnwahsreprasiiph Dldpftchtiera-kasmingivakdlodekiivperpresere GTsrftmtstranrekriasyistlrhedgoldleftypglrgsphotemfteli EELLFAFRKEALLTmrprlllsaavsgvphivorstlgrllpfinvlsydlhgs MEKFTGHNSPLFSI,PEDPKSSAYAMNYRKLGAPSEKLIMGIPFYGRTFTLKASKNG LOATAIGPASPGKYTKOAGFLAYETEISEFWGAKKHWIDYQYVPYANKKEWGYDDA ISFSYKAWFIRREHFGGAAVWTLDMDDVRGTFCGTGPFPLYYVNNDILVRAEFSSTSL EQFWLSSAVNSSSTDPBKLAVTKAWTFDIKILPPGGEAGVTELHGKCENMTIPFRTTI UTPKETVSIGKHTVALGEKTEITGATTMTSVGHOSMTPGEKALTPVGHOSELPGKKT LTPVGHOSVTTGGKTLISVGYHSVTPGEKTLTPVGHPSVTPVSHQSVSEGGMTMTPH EQTETLAQNTMAPRKAVAHEKYTYSGEKTLTPVBGGTVPLRGEYLTSETGTHPQDG" EGTOი 531 g 566 t

BASE COUNT ORIGIN Query Match Best Local S Matches 36 510 319 690 679 630 619 570 559 499 450 439 390 379 330 270 259 213 199 153 139 y Match 5.5%; Local Similarity 58.5%; hes 363; Conservative 93 79 acaggacataatagccccct 698 gctgctgtttctggggtcccacacatcgtccaaacatcctatgatgtgcgctttctagga ctcctgtttgccttccggaaggaggcactgctcaccatgcgcccaaggctgctgctgtct 558 CCAGGAAGCCAGGGGAGCCCTGCCGTAGACAAGGAGCGCTTCACAACCCTGGTACAGGAC cctggactaagaggcagcccatgcatgaccggtggacttttctcttcttaattgaagag AGCACTCAGAAGTTCACAGATATGGTAGCCACGGCCAACAACCGTCAGACCTTTGTCAAC GGCCTGAAGAAGATGAATCCCAAGCTGAAGACCCTGTTAGCCATCGGAGGCTGGAATTTC Baactamaggagaggaacagagagctgaaaacactgctgtccatcggcgggtggaacttt 318 CCCAAGGACTTGGACCCCAGCCTTTGCACCCACCTCATCTACGCCTTCGCTGGCATGACC ccccatgacctggacccctttctctgcacccacctgatatttgcctttgcctcaatgaac 198 GCAGCGGTTCCAGCTGGGCAGACCTATGTGGATGCTGGATACGAGGTGGACAAAATCGCC TCGGCCATCAGGTTTCTGCGCAAATACAGCTTTGACGGCCTTGACCTTGACTGGGAGTAC ACGGGACATAACAGCCCCCT 559 ß Score 91; DB 67; Length 2228 Pred. No. 9.79e-59; 0; M1smatches 254; Indels Length 2228; ω '' Gaps 618 498 449 378 689 678 389 329 212 629 569 509 ۲.

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Search completed: Sun Jun 29 20:45:12 1997 Job time : 1558 secs.

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Release 2.1D John F. Collins, Blocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Tabular output not generated. Sun Jun 29 20:45:32 1997; MasPar time 177.88 Seconds 861.257 Million cell update updates/sec

Perfect Score:
N.A. Sequence:
Comp: Description: (1-1656) from US08663618A.seq

>US-08-663-618A-3

Title:

1656

Scoring table: TABLE default Gap 6

Nmatch

STD

Dbase 0;

Query 0

121476 segs, 46255616 bases × N

Post-processing: Minimum Match Listing first 0% 45 summaries

Database: n-geneseq26

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.577; Variance 5.573; scale 1.719

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q70465 Q70466	Q70467 Q70469	Q51746 Q70468 N81164	Q90444 N81164 Q51746	Q90443 Q90442 Q10572	Q85245 N81756 Q10572	ID
Generic DNA sequence	Generic DNA sequence Generic DNA sequence	Oligonucleotide probe Generic DNA sequence Base substituted E.co	Hamster oviduct speci Base substituted E.co Oligonucleotide probe	Murine oviduct specif Bovine oviduct specif Human Natriuretic Pep	YKL-40 gene. Gene encoding polypep Human Natriuretic Pep	Description
4.64e-07	1.26e-07 1.26e-07	1.60e-10 3.39e-08 3.39e-08	4.37e-26 5.90e-16 2.64e-12	$\omega \omega \omega$	5.39e-101 2.21e-69 1.24e-42	Pred. No.

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Query Match 10.6%; Best Local Similarity 63.5%; Matches 697; Conservative

Score 176; DB 13; I Pred. No. 5.39e-101; 0; Mismatches 377;

Length 1681; Indels 24;

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ALIGNMENTS

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RESULTANCE OF THE PROPERTY OF 
Use of YKL-40 and anti-YKL-40 antibodies - for developing prods. for diagnosis prognosis and therapy of diseases involving connective tissue degradation.
Disclosure; Page 66-67; 88pp; English.
YKL-40 (40 kDa) was purified from human osteosarcoma MG63 cells.
The N-terminal sequence is shown in R70745; the full coding region of the YKL-40 gene is given in 082245. Homology of the N-terminal and 2 internal peptides (R70746-47) with a bacterial polysaccharide hydrolase suggests that YKL-40 degrades polysaccharide connective tissue. YKL-40 degrades polysaccharide connective tissue. YKL-40 is a marker of e.g. metastatic breast cancer and inflammatory or degenerative joint diseases.
Sequence 1681 BP; 401 A; 503 C; 421 G; 356 T;
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Q85245 standard; cDNA; 1681
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08-JUL-1994; U07754.

09-JUL-1993; US-089989.

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Best Local
Matches 2
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Q10572 standard; DNA; 1047 BP.
Q10572;
Q9-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB; ANP; BNP; CNP; kidney failure; hhyperaldosteronism; glaucoma; guanyl c
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J63032898-A.
30-JAN-1988; 167518.
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WPI; 88-068419/10.
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such as immune response etc.
Disclosure; p; Japanese.
Polypeptide encoded is involved
response, cell growth and activa
Sequence 966 BP; 238 A; 28
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                                                                      extracellular domain binds natriuretic peptides
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Similarity 66.1%;
269; Conservative
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Best Local Similarity
Matches 106; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1; 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodm. of the protein, opt. after being mutated to produce NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein has a mol wt. of 115 kD (calculated matriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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23-JUN-1989; US-370673.
(GETH) GENENTECH INC.
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Modified -site 244..246
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Modified -site 195..1
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Modified -site 161..163
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91-036711/05.
                             AGACAAGGAGC-GCTTCACAACCCTGGTACAGGACTTGGCCAATGCCTTCCAGCAGGAAG
                                               rnvnkmngrryhgvtgnvvmdknndrntdnvnwamgdndsgdnnnaahysganknnwwtg
                                                                                     AGCTTTGACGGCCTTGACCTTGACTGGGAGTACCCAGGAAGCCAGGGGAGCCC-TGCCGT
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; Pred. No. 1.24e-42;
279; Mismatches 603;
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Query Match
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15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE K
WPI; 95-190179/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine oviduct: Murine oviduct: MOGP; ds.
                                                                New DNA encoding an oviduct-specific glycoprotein recombinant protein production in high quantities. Claim 1; Pages 11-14; 22pp; Japanese.
090443 encodes R73992 murine oviduct specific glycombinan be used for the commercial recombinan MOGP in high quantities.
Sequence 2504 BP; 678 A; 616 C; 538 G;
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58.58;
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15-ADG-1994; 214227.
19-AUG-1993; JP-227881.
19-AUG-1993; JP-27881.
(KINO-) KINOSED PEPTIDE K
WPI; 95-190179/25.
P-PSDB; R73991.
New DNA encoding an ovidurecombinant production production 1; Pages 7-9; 22pp;
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Bovine oviduct
BOGP; ds.
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/note= "START
sig_peptide
/*tag= b
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Key
CDS
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Q90442 standard;
Q90442;
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ct specific glycoprotein cDNA.
ct specific glycoprotein; reco
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                                                                                                            Location/Qualifiers 2..1615
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                                                                                                                                                                   CDNA
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oviduct-specific glycoprotein production in high quantities 22pp; Japanese.
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/label= extracellular domain
/note= "binds natriuretic peptides
Domain 456..456
/label= transmembran-
                                                                                                                                                                                                                 LT 6
Q10572 standard; I
Q10572;
Q10572;
09-APR-1991 (fir
                                                                                                                                                                    09-APR-1991 (first entry)
Human Natriuretic Peptide Receptor B.
NPRB, ANP, BNP, KONP, kidney failure;
hyperaldosteronism; glaucoma; guanyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O90442 encodes R73991 bovine oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. BOGP in high quantities.
Sequence 1994 BP; 445 A; 536 C; 520 G; 493 T;
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| Similarity 57.9%;
359; Conservative
transmembrane
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Tahes 258;
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23-JUN-1989; US-370673.
(GETH ) GENENTECH INC.
Chang M, Goeddel D, Lowe D
WPI; 91-036711/05.
N-PSDB; Q10324.
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Modified -site 24..26
/label= N-glycos_site
/label= N-glycos_site
35..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natriuretic protein receptor B - for diagnosis and treatment of kidney failure, heart failure, hyperaldosteronism, glaucoma etc. Claim 3; Fig 1: 49pp; English.

The sequence was derived from the DNA encoding natriuretic peptide receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce MPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr-114,952). The protein (or variants) can be used in treatment of natriuretic peptide disorders, and also to isolate peptides using affinity chromatography. Antibodies with affinity for NPRB can
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wodified -site 161..163
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25-APR-1994; 214227.
15-AUG-1993; JP-227881.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO WPI; 95-190179/25.
                                                                                                                                                                                     New DNA encoding an oviduct-specific glycoprotein - useful frecombinant protein production in high quantities. Claim 1; Pages 16-18; 22pp; Japanese - 090444 encodes R73993 hamster oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. Graph in high quantities. Sequence 2366 BP; 602 A; 574 C; 573 G; 617 T;
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30-MAR-1988;
03-APR-1987;
                                                                                                                                                                                                                                                        E.coli beta-galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to the stranded template and an oligonucleotide with the sequence at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are completed to forms that can amplified and them expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of where correct singularly in a suitable control of the control of the sequence covers all 176 difft base substitutions, most of where correct singularly in a suitable control of the sequence covers all 176 difft base substitutions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUSO) SUOMEN SOKERI OY. Lehtovaara P. Knowles J. WPI; 88-279927/40.
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galactosidase alpha-fragment; base substitutions;
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larity 15.4%;
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Shank DD, Spears PA,
WPI; 93-378844/48.
I New oligo:nucleotide probes sp
sheection and amplification of
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EP-571911-A.
01-DEC-1993.
24-MAY-1993;
26-MAY-1992;
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EP-571911-A.
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Q51746 standard;
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Shank DD, Spears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes
detection and amplification
                                                                                                                                                                                    oligonucleotide probe WK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. see also Q51735-45 and Q51747-59.

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
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Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide;
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Oligonucleotide probe MK14-A
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Pred. No.
45; Misma
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Pred. No.
47; Misma
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CCTGCCCAAGGACTTGGACCCCAGCCTTTGCACCCACCTCATCTACGCCTTC

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RESULT RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing as generic DNA sequence used to generate random TSAR (Totally CO 70468 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be crepresented as follows: X(NNB)11(TGC)(NNB)52(NNB)10Y. X CC and Y are flanking restriction sites (X is not the same as Y) that are contained for the specific peptides generate by these generic sequences are shown in Q70466-68. CC Other specific peptides generated by these generic sequences are shown in Comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain with CC comprising at least two functional regions - a binding domain that is competite between the 2 domains. The oliquoucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs CC confers some degree of conformational rigidity to the peptides. The TSARs concentration of macromolecules, eg. metal ion, calcium the contains of post of the conformation of the context the need concolonal or polyclonal antibodies and therefore circumvent the need concolonal or polyclonal antibodies and therefore circumvent the need concolonal or polyclonal antibodies and therefore circumvent the need concolonal concolon
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18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
LT 12
N81164 standard; DNA; 204 BP.
N81164;
08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding ceffector domain; concateneated heterofunctional protein; links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q70468 standard;
Q70468;
Q5-APR-1995 (fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNC-) UNIV NORTH C. Fowlkes DM, Kay BK; WPI; 94-279739/34.
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Pred. No.
34; Misma
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(see
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treatment; generic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Random point mutations were introduced into the alpha fragment of E. coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.

See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 1
                                             (UYNC-) UNIV NORTH Fowlkes DM, Kay BK WPI; 94-279739/34. P-PSDB; R65153.
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(SUSO) SUOMEN SOKERI OY.

Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikaine
Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikaine
WPI; 88-279927/40.

Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer
by prepn of single stranded template, annealing a primer.
                                                                                                                                            18-AUG-1994;
01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
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30-MAR-1988;
03-APR-1987;
                                                                                                                                                                                                                                                                                                  sequence
comments)
                                                                                                                                                                                                                                                                                                                                                                                                                                       currect; rapid;
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-ARR-1995 (IIISt eury)
Generic DNA sequence to generate a random TSAR petide lir
Generic DNA sequence to generate a random TSAR petide lir
TSAR; totally synthetic affinity reagent; synthetic; bind
effector domain; concateneated heterofunctional protein;
effector domain; concateneated heterofunctional protein;
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                                                                                                                                                                                                                                                                         WO9418318-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                       of
proteins or peptide(s) which bind a ligand recombinant vector library expressing fusio
                                                                                                                  ; U00977.
; US-013416.
; US-176500.
; US-189331.
V NORTH CAROL
                                                                                                Kay BK;
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llarity 11.5%;
Conservative
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US-034819.
                                                                                                                                                                                                                                                                                                                       sequence represents 'Z';
5, 9 or 12 nucleotides (se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                          CAROLINA
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Pred.
49; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
3.39e-08;
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  fusion
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proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
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RESULT.

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A C
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PS Disclosure; Page 35, 255pp; English.
CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides.This generic formula can also be
CC represented as follows: X(NNB)16(TGC)(NNB)1Z(NNB)16(TGC)(NNB)1Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specific further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65131-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the Z domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
Ci n, or flanking, the unpredicted or variant residues. These residues
CC confers some degree of conformational rigidity to the peptides. The TSARs
CC comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC complex methods of hybridoma formation or in vivo antibody production.
CC The TSARs are easily characterised and have designed activity allowing
CC direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLI
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.

Q70469 is a generic DNA sequence used to generate random TSAR peptide This generic formula can be represented as follows: X(TGC)(NNB)10-(TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other generic sequences are shown in Q70465-68. Other specific peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do effector domain; concateneated heterofunctional protein; linker direct; rapid; detection; screening; treatment; generic; ss.
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18-AUG-1994.
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llarity 4.8%;
Conservative
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32; M
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1.26e-07
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; ss.
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            PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PT comprising a binding domain and an effector domain
PT comprising a binding domain and an effector domain
PT comprising a binding domain and an effector domain
PT comprising a binding domain and an effector domain
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PT comprising a binding testiction sites (X is not the same as Y) that are
PT comprising a binding restriction sites (X is not the same as Y) that are
PT comprising a binding restriction sites (X is not the same as Y) that are
PT comprising at least two functional proteins or peptides,
PT comprising at least two functional regions - a binding domain with
PT comprising at least two functional regions - a binding domain with
PT comprising a light a second effector peptide portion that is
PT comprising a binding domains. They may further comprise a linker
PT comprise a light active. They may further also designed so
PT comprise a companies of the peptide portion of that is a companies and the period of the per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc generated by these generic sequences are shown in R65150-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and cc ascond effector peptide portion that is chemically or biologically cc The oligonucleotides are also designed so that the expressed peptide cc contains 2 or 4 cysteine residues positioned in, or flanking, the cc unpredicted or variant residues. These residues confer some degree of cc conformational rigidity to the peptides. The TSARs or compans. comprising ca TSAR binding domain can be used in vivo to deliver a chemically or cc biologically active moiety, eg. metal ion, radioisotope, peptide, toxin cc rezyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma cc characterised and have designed activity allowing direct and rapid
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Matches
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01-FEB-1993; US-013416.

01-FEB-1993; US-176500.

30-DEC-1993; US-176500.

31-JAN-1994; US-189331.

(UYNC-) UNIV NORTH CAROL

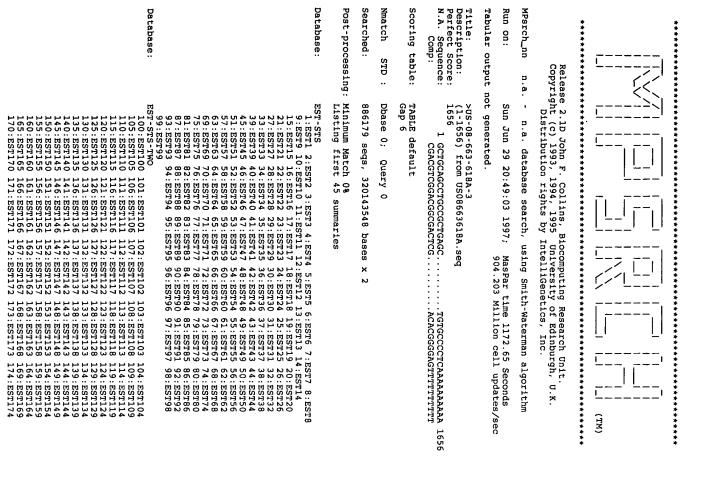
FOWLKES DM, Kay BK;

WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity regent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of comments) "
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Q70465 standard;
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Similarity 6.3%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               R65150 and R65151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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32; N
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Search completed: Sun Jun 29 20:48:37 1997 Job time: 185 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or companies comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                            215 CCACCAGCTGAGCACCACTGAGTGGAATGACGAGACTCTCTACCAGGAGTTC 266
                                                                                                                                                                                                                                                   155 CAAGGACTTGGACCCAGCCTTGCACCTCATCTACGCCTTCGCTGGCATGACCAA 214
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Statistics: Mean 11.532; Variance 2.180; scale 5.290

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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DEFINITION
ACCESSION
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Best Local S
Matches 38
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Holman,M., Hultman,M., Kucaba,T., Le,M., Lenny Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., T. Waterston,R., Williamson,A., Wohldmann,P. and washU-Merck EST Project
                                                                                                         gcccagcctcaaagctggacttggaggggctttan-gactcaattccaggtgcagcattt
                                                                                                                                                                    GAGGGGCACAAACCAAAGATTTATTTTGCAAGTGAAAGGGGCCAGCCCAGGAGACCCAGAA 1587
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                                               gcagganttgctgaacaccaggcctntcgggcagcttt-ctgnaacaccngccccgntgc
                                                                                                                                                     ANAAGGAAGGCAAGGCTGAGAGCAGAAAGCCTGGATAAAGGAAGACCACAGAAAGGCCTG
                                                                                                                                                                                                                                  aaaaggaaggcaaggctgagagcagaaagcctggataaaggaagaccacagaaaggcctg 125
acaactgtagaagctggaccgttcccgaggnttgggatagagcccatcagcttt-ccctg 362
                              GCAGGAGTTGCTGAACACCAGGCCTGTCGGGCAGCTTTGCTGGAACAGCCGCCCCGCTGC
                                                                                         GCCCAGCCTCAAAGCTGGGACTGGAGGGGCTTTAGCGACTCAATTCCAGGTGCAGCATTT 1407
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EST.
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vector-pBluescript SK- host-SOLR cells (kanamycin resistant)
primer-21m13 Rsitel-EcoRI Rsite2-XhoI Normall lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GARITCGCCACGAC-3', 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
WashU_Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ye31g05.s1
T94579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stops: 241
ce: IMAGE Consortium, LINL
clone is available royalty-free through LLNL; contact the
Consortium (info@image.llnl.gov) for further information.
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/clone="119384"
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Pred. No. 0.00e+00;
0; Mismatches 18;
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T., Tan,F.,
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Matches 37
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               ttacagccttgccttcctggggttttccctggggggccgcaatctgggntccttgcaggc
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1 (bases 1 to 405)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. washU-Merck EST Project

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU-Merck EST Project
Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=119384 library=Stratagene lung (#937210)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsite1=EcoRI Rste2=XhoI Normal lung tissue from
year old male. Cloned unidirectionally. Primer: Oligo dT. Avera
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ye31g05.rl Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops:
Source: IMAGE Consortium, LLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free the IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                             h 14.8%;
Similarity 91.6%;
371; Conservative
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/clone="119384"
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Mismatches 14;
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RESULT REPORT OF THE PROPERTY 
RESULT 4
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Best Local
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Stanford University School of Medicine Department of Genetics,
M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689
M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689
Email: myers@shgc.stanford.edu Primer A: AAAGCCTGGATAAAGGAGACC
Primer B: GCTGCACCTGGAATTGAGTC STS size: 150 PCR Profile: Initial
incubation: 94 degrees C for 90 seconds Denaturation: 94 degrees C
for 15 seconds Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds PCR Cycles: 30 Thermal
Cycler: Perkin Elmer 9600 Protocol: Template: 25 ng Primer: each 1
UM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total vol: 10
ul Buffer: MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 20 mM pH: 8.3
Prepared with primer pairs derived from T94579--Merck/UniEST.
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primer_bind
Sequence 241
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Eukaryota; Animalia; Metazoa; Chordata; Vertebrata;
Theria; Eutheria; Primates; Haplorhini; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-1996 (Rel. 49, 05-OCT-1996 (Rel. 49, human STS SHGC-17364.
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1 Similarity 97.0%;
230; Conservation
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91..112
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78 A; 53 C; 77 G; 30 T;
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SHGC-17364
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Pred. No. 0.00e+00;
0; Mismatches 5;
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Hominidae.
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Stanford University School of N
Department of Genetics, M-344,
Tel: 4157259887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer A: AAAGCCTGGATAAAGGAAGACC
Primer B: GCTGCACCTGGAATTGAGTC
STS size: 150
PCR Profile:
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230; Conser
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High quality sequence stops: 323
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ost Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Ho (bases 1 to 405)
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yp05a12.rl Homo sapiens cDNA clone 186526 5' similar to gb:M80927
CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
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CARTILAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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VV29c01.rl Homo sapiens cDNA clone 244128 5' similar to gb:M80927
CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN):
                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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Pred. No. 1.34e-98;
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  CTCTCCACATCAAAGCCCACCCACT-GGTTGTCCCGGAAGATGTAGGGCCACCTTCTG
                              ctcttcacatcatcatagcccacccacttggttccccttgactncgtaggggacctgctg 429
                                                                                             GCCCAGACCATGGCCCCGCCCAGTCCCTTCTGCTTCAGATAGCTGACCTTGGTTTTGAAG 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-Merck EST Project
Washington University Schoo
4444 Forest Park Parkway, B
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 53)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Washu, Merck, EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human clone=81581 library-Stratagene lung (#937210)
vector=pBluescript SK- host-SOLR cells (kanamycin resistant)
primer=-21m13 Rsite1=EcoRI Rsite2-XhoI Normal lung tissue from a 7
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High qality sequence stops: 30 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.sl Homo sapiens of SECRETORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/clone="81581"
123 c 136 g 128
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Best Local Similarity 70.1%;
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gaccagatcatggctcctcccaggtttaaattctttaagaactgaaccttggtctccata 369
                                         TGGATGAGGGGGTATCGGCCCTGGTTGCAGGAGAAGCCCGGCAAAGTCATCTAAGTCCAGT 1103
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Primer B:
STS size:
                                                                                                  131;
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Fax: 617 252 1902
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STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST
                                                                                                                                                                                                                                                                                          Derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
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Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.0
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KCl: 50 mM
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ctgggcaggtgtagtggtcttgctgcttctccagggaggatctgcctacaaactggtttg 128
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                                                                                                                           156;
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CARTILAGE G
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
WashIngton Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
High quality sequence stops: 268
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                      4.3%;
Similarity 65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human clone=257753 primer-T7 library=Soares placenta 8to9weeks 2NbHP8to9W vector=pT7T3D (Pharmacia) with a modified polylinker
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                                                                                                                                                                                                       /organism="Homo sapiens"
/clone="257753"
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81 c 68 g 6
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GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                            Score 71; DB 79; Lengum Jan., Pred. No. 5.83e-85; and matches 80; Indels
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257753 5' similar to gb:M80927
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Best Local Similarity 69.2%;
Matches 137; Conservative
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                                                                                             acaccaactggtcccagtaccgggaaggcaatgggagctgcttcccagacgccctcgacc
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similar to
W51302
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 336)
Marra, M.: Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 148.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pCMV-SPORT2; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. pCMV-SPORT2
                                                                                                                                                                                                                                                                                                           /clone="304743"
/clone=lib="Life Tech mouse brain"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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Life Tech
gb:x93035
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                                                                                                                                                                                                  Score 71; DB 169; Pred. No. 5.83e-85; 0; Mismatches 60;
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Best Local Similarity
Matches 127; Conser
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                                                                              agctgg-cgggcgcatggtatgggccctngacctggatnacttncagggctccttctgcg 192
                                                                                                                                       gggtaggatacgacgaccaggaaagcgtcaaaagcaaggtgcagtacctgaaggacaggc 133
                                                                                                                                                                                    GGGCCACCAAACAGAGAATCCAGGATCAGAAGGTGCCCTACATCTTCCGGGACAACCAGT 1017
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                              gccagg
                                                             GACTGGGCGGGCCATGGTCTGGGCACTGGACTTAGATGACTTTGCCGGCTTCTCCTGCA 1137
                                                                                                                       GGGTGGGCTTTGATGATGTGGAGAGCTTCAAAACCAAGGTCAGCTATCTGAAGCAGAAGG 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stops: 84
Source: IMAGE Consortium, LLNL;
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and M.Fatima Bonaldo.
                                198
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                                                                                                                                                                                                                                                4.0%;
larity 68.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/clone="160921"
1 80 c 70 g 5:
                                                                                                                                                                                                                                                                                                                                                                        1..266
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Pred.
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                                                                                                                                                                                                                                              re 66; DB 35; I
d. No. 2.27e-75;
Mismatches 58;
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Louis,

MO 63108

58;

Indels

Gaps

Length 266;

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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 266)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                   200 DP MRNA EST 07-JUL-1995 y142f01.rl Homo saplens cDNA clone 160921 5' similar to gb:M80 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
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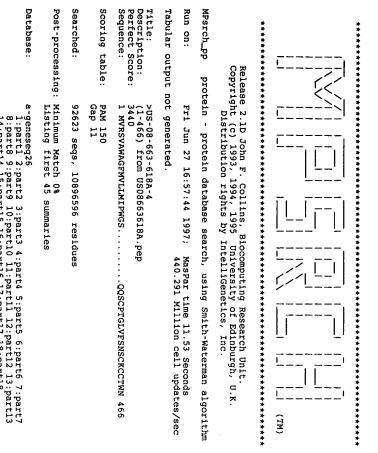
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BASE COUNT
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Best Local
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Local Similarity 68.3%;
                                                                                                                                                                                                             acaccagctggtcccagtaccgggnangcgatggggagctgcttcccagatgcccttgacc 244
                                                                                                                                          gnntcctctgtacccacatcatctacagctttgccaatataagcaac
                                                                                                                                                                                          TCACCAACTGGGCCCAGTACAGACAGGGGGGGGGGCTCGCTTCCTGCCCAAGGACTTGGACC 168
                                                                                                                        CCAGCCTTTGCACCCACCTCATCTACGCCTTCGCTGGCATGACCAAC
306 bp mRNA EST 26-APR-1996 ma47907.rl Soares mouse p3NMF19.5 Mus musculus cDNA 5' similar gb:M80927 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HIMAN).
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yj79cl2.rl Homo sapiens cDNA clone 154966 5' similar to gb:M8C
CARTILAGE GLYCOPROTEIN-39 PRECURSOR (HUMAN);.
R55530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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High quality_sequence stops: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/clone="154966"
106 c 109 g 8
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                                                                                                                                                                                                                                                                                                                             Score 65; DB 134;
Pred. No. 1.81e-73;
0; Mismatches 53
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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Similarity 72.1%;
98; Conservative
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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No. 4.65e-64;
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Matches 98; Conservative
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High quality sequence stop: 172.
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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The WashU-HHMI Mouse EST Project Unpublished (1996)
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Mus musculus
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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Fax: 314 286 1810
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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<1..>36 85 g 67 t
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:1stics: Mean 36.091; Variance 158.898; scale 0.227	- 11
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116 R86905 Murin, 2 R07575 Gluco, 2 R07575 Gluco, 1 P81181 Seque, 4 R21521 Alpha 9 R47259 Pre-p, 18 R98125 Human 5 R26999 NOVell 11 R70752 YKL-4 11 R70752 YKL-4 11 R70752 Prote 9 R47264 Pre-p, 2 R07311 Human 6 R32904 Human 7 R36735 Prote 9 R47264 Pre-p, 2 R07311 Human 6 R32904 Human 7 R36735 Human 7 R36735 Human 7 R36735 Human 7 R36735 FixD 17 R99248 Limnan 18 R94503 1-acy, 16 R87724 Limnan 18 R94503 1-acy, 16 R87724 Human 18 R94503 1-acy, 16 R87724 Human
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Murine BMP-9. Murine soluble epoxid Glucoamylase encoded Sequence of glucoamyl Alpha galactosidase. Pre-pro-VGR1. Human lymphocyte cell Novel type III RTK en YKL-40 internal pepti YKL-40 internal pepti MuTu putative oncogen Protein encoded by Mu Pre-pro BMP6. Human BOMP-6 peptide s Human BMP-6. Sequence encoded by t sequence encoded by t FixD nitrogen fixatio Human EGF receptor su 1-acylglycerol-3-phos Full length meadowfoa Limmanthes 2-acyltran Bacillus stearothermo Human antihaemophilic

ALIGNMENTS

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Query Match 39.1%; Score 1344; DB 14; Length 668; Best Local Similarity 48.3%; Pred. No. 2.56e-114; Matches 185; Conservative 84; Mismatches 103; Indels 11	recombinant protein production in high quantities. Claim 4; Pages 16-18; 22pp; Japanese. Q90444 encodes R73993 hamster oviduct specific glycome cDNA can be used for the commercial recombinant HOGP in high quantities.	Peptide 19668 /label= mat_peptide J07107979-A. 25-ARR-1995. 15-AUG-1994; 214227. 19-AUG-1993; JP-227881. (KINO-) KINOSEI PEPTIDE KENKYUSHO KK. WPI; 95-190179/25. N-PSDB; 090444.	RESULT 1 ID R73993; standard; Protein; 668 AA. AC R73993; pr 10-JAN-1996 (first entry) DE Hamster oviduct specific glycoprotein. KW Hamster oviduct specific glycoprotein; recombinant production; KW HOGP. OS Cricetulus griseus. FH Key Location/Qualifiers FT Peptide 1.18 Peptide 1.18 FT Peptide 1.18
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WPDI; 95-190179/25.
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190; Conser
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19..537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.98;
llarity 50.18;
Conservative
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ct specific glycoprotein.
ct specific glycoprotein;
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Pred.
81; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1339;
No. 7.
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7.77e-114;
ches 101;
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N J07107979-A.

D 25-APR-1995.

F 15-AUG-1994; 214227.

F 19-AUG-1993; JP-227881.

R (KINO-) KINOSEI PEPTIDE KENKYUSHO KK.

R WPI; 95-190179/25.

R N-PSDB; 090443.

S Claim 4; Pages 11-14; 22pp; Japanese.

C 190443 encodes R73992 murine oviduct specific glycoprotein (MOC 090443 encodes R73992 encodes R73994 encodes R73994 encodes R7394 encodes R73994 encodes R73994 encodes R73994 encodes R73994 encodes R73994 encodes R73994 enco
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Best Local
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/label=
19-OCT-1990 (first entry)
Polypeptide involved in pro
Immune response; cell grow
J63032898-A.
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Murine oviduct specific glycoprotein.
Murine oviduct specific glycoprotein;
                                                                                                         P81342 standard; P81342;
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                                                                                                                                                                                                                                                                        W-KGATKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYSFDGLDLDWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nlqdenvlypefnklkernrelktllsiggwnfgtsrftamlstlanrekfidsvisflr 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
190; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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llarity 49.0%;
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                                                    protective
                                                                                                                                  321
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Pred. No. 1.39e-112;
82; Mismatches 107;
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RESULT AND RESULT AND

Key Bos BOGP

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Best Local
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                                                                                                                                                                                       17-AUG-1993; EP-202425.
(MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
Apotheker de Groot M, Bol
Melchers LS, Ponstein AS,
        New plant protein having endo-chitinase activity - used in antifungal compans. and to develop transformed plants which are less susceptible to fungal infection.

Claim 3; Page 19-20; 43pp; English.

Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN tobacco plants with a probe derived from PROB40 (a partial Cluster-A cDNA clone) resulted in the isolated of 11 positively hybridising clones. Analysis revealed that all were identical and corresp. to Cluster-A cDNA. The nt sequence of clone cA-3 is given in 082973/R70025. This clone lacks 7 codons of the 5' part of the order. The CDNA clone was completed by performing a PCR reaction on clone cA-3 with primer T7 (082794) and primer P1 (08275). A partial AA with primer T7 (082794) and primer P1 (08275). A partial AA
                                                                                                                                                                                                                                           22-FEB-1995.
17-AUG-1993;
17-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1995 (first entry)
Tobacco chitinase encoded by tol
Tobacco; chitinase; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DAIN) Dainippon Pharm KK. WPI: 88-068419/10. P-PSDB; P81342. New polypeptide and DNA en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; p; Japanese.
This polypeptide is involved in protective mechanisms such as response, cell growth and activation of protective functions.
Sequence 321 AA;
                                                                                                                                                                                                                                                                                                           /note= "Determined by protein Misc_difference 216..241
                                                                                                                                                                                                                                                                                                                                    /note= "not present in
Misc_difference 182..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide and DNA encoding it - mechanisms such as immune response etc
                                                                                                                                                                                                                                                                                  /note= "Dete
EP-639642-A.
                                                                                                                                                                                                                                                                                                                                                               Misc_difference
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16-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-1988
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                                                                                                                                                                95-083454/12.
>B; Q82973.
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:|::|:: ||::||::|:|||||:: ||:::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKYSFDGLDLDWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG
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                                                                                                                                                                                                                                                                                                                                                                         signal peptide
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JP-167518.
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                                                                                                                                                                                         JF, Cornelissen BJC,
Sela-buurlage MB;
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Pred.
66; M
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al; fungicide; Cluster-A.
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No. 2.43e-72;
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TMV-infected tobacco
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Best Local
             New plant protein having endo-chitinase activity - used in antifungal compsns. and to develop transformed plants which are less susceptible to fungal infection.

Claim 3; Page 25-28; 43pp; English.

Screening of lambda ZAP cDNA library of TMV-infected Samsunn NN cobacco plants with a probe derived from PROB40 (a partial Cluster-cDNA clone) resulted in the isolated of 11 positively hybridising clones. Analysis revealed that all were identical and corresp. to cluster-A cDNA. The sequence of CDNA clone cA-3 is given in 082973/ R70025. A genomic library of N. tabacum was screened using the Cluster-A cDNA insert of clone cA-3 as a probe (see 082977, 082978) The complete nt. sequence of Cluster-A cDNA including the deduced primary structure of the Cluster-A protein the 5' and 3' UTR region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R70029
                                                                                                                                                                                                         (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN
Apotheker-de Groot M, Bo
Melchers LS, Ponstein AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was obtd. and found to deduced from the cDNA. Sequence 371 AA;
                                                                                                                                                                                            Melchers LS, Ponstein WPI; 95-083454/12.
                                                                                                                                                                                                                                                                                                                           /label- Determined by sequencing Misc_difference 222...247
                                                                                                                                                                                                                                                                                                                                                     /note= "cDNA encodes additional Misc_difference 188..201
                                                                                                                                                                                                                                                                                                                                                                              /label= signal peptide
Misc_difference 28..29
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1995 (first entry)
                                                                                                                                                                                 N-PSDB; Q82976
                                                                                                                                                                                                                                                              17-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco cluster-A
Tobacco; chitinase
                                                                                                                                                                                                                                                                           17-AUG-1993;
                                                                                                                                                                                                                                                                                                                /note=
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chitinase; antifungal; fungicide; Cluster-A
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in Q82976/R70029. Comapri
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No. 3.72e-43;
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  including the deduced the 5' and 3' UTR regions aprison of the cDNA
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                                                                                                                                                                                                                                                                                                                                  (Eng).
(Eng).
(Eng).
(Example 8; Page 45; 62pp; English.
Example 8; Page 45; 62pp; English.
(P8144 encodes R63441 the Trichoderma harzianum P1 endochitinase, over the second of the sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORR ) Cu...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichoderma harzianum useful in biological c
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14-APR-1993; US-045269.
(CORR) CORNELL RES FOUND
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larity 36.4%;
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5.10e-42;
ches 95;
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Disclosure and Claim 8; Page 39-40; 64pp; French.
The sequence coding for wheat germin, a protein induced during germination of wheat, is a preferred example of DNA coding for a protein able to degrade oxalic acid. Such DNA can be coupled to a sequence of interest, e.g. one coding for enzymes which confer resistance to pathogens (esp. endochitinases). Plant calli which have been successfully transformed by the sequence of a mature endochitinase; the sequence was previously disclosed in EP-531218.
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(ERAP ) SOC NAT ELF AQUITAINE.
Grezes-Besset B, Grison R, F
WPI; 94-217870/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of gene encoding oxalic acid
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gcysydpstkelisfdtpamistkvswlkgkglggsmfw
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Aphanocladium album n
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(SNFI ) ELF SANOFI.
(ERAP ) SOC NAT ELF AQUITAINE.
Legoux R, Leguay
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N-PSDB: Q37711, Q37712.
Recombinant DNA encoding fungal endo:chitinase - useful
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Claim 1; Fig 1; 75pp; French.
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06-SEP-1991; FR-011072.
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larity 36.6%;
Conservative
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pathogen resistance.
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64; Mismatc
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.79e-41;
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RESULT AND ACTION OF ACTIO
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Vibrio 1...
WO9625424-A1.
22-AUG-1996.
13-FEB-1996; U02332.
R 13-FEB-1995; US-386727.
OR 13-FEB-1995; US-386727.
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EP-531218-A.
10-MAR-1993.
04-SEP-1992; 402414.
06-SEP-1991; FR-011072.
(SNFI ) ELF SANOFI.
(ERAP ) SOC NAT ELF AQUITAINE.
Chitin biosynthetic enzymes end I, exo I and exo II - are periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) aryl beta-N-acety:gluco:amidase(s), respectively example 4; Page 79-82; 101pp; English.

Periplasmic chitodextrinase (W02156), periplasmic Beta-N-acety1glucosaminidase (W02157) and aryl Beta-N-acety1glucosaminidase (W02158) can be used to produce chitologoaccharides with the structure (GlcNAc)n where n is 2 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 11
W02159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This mature protein from the filamentous fungus Aphanocladium album has endochitinase activity and is used to control pathogens such as fungi, bacteria, arthropods and nematodes on plants. Recombinant DNA comprising the endochitinase coding sequence is specifically intended for transforming Nicotiana tabacum, Helianthus
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                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protecting plants against fungi,
Claim 22; Page 60-61; 75pp; Fren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplasmic chitodextrinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble chitinase.
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Pred. No. 8.03e-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; periplasmic Beta-N-acetylglucosaminidase;
chitin; oligosaccharide; catabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
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encoded b
all genes
Sequence
                                                                                                                                                                                        plant cell conty. signal sequence of chitinase A gene - for secretion of foreign polypeptide, esp. chitinase A for protection against pathogenic fungi and nematodes.

Disclosure; Fig. 1A-1C; 20pp; English.

Serratia marcescens QMB1466 genomic DNA was partially digested,

Ligated into vector pLAFR1, packaged into lambda phage particles,
and used to transfect Escherichia coli DH1 (ATCC 33849) cells;

Plating on chitin medium was used to screen for chitinase activity.

Clone C12 (ATCC 67152) was isolated. Its sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-1986;
09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-035648/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1984; US-593691.
18-JUL-1986; US-888033.
09-JUL-1990; US-550253.
(DNAP ) DNA PLANT TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitinase A; protein secretion; biological control transgenic plant; chitin; plant pathogen; nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones JDG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1984;
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                                                                         Local
                                                                                                  Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protection; pCHIT1251.
atia marcescens QMB1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vnnrmgagweggydetaeapyvfkastgdlisfdndrsvkakggyvlanglgglfaweid
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                                                  Similarity
92; Conser
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94; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suslow T;
                                                                                                                                                                           the
                                             11.4%;
larity 28.5%;
Conservative
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larity 31.0%;
Conservative
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                                                                                                                                                                      protein sequence
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                                               Score
Pred.
80; M
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Pred.
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                                             re 392; DB 12; L
1. No. 3.09e-24;
Mismatches 126;
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No. 5.
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5.32e-31;
hes 104;
                                                                                                                                                                    Its sequence is given 
nce in R64823.
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                                               Indels 25;
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Best Local
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US5290687-A.
01-MAR-1994.
26-MAR-1984; 593691.
26-MAR-1984; US-593691.
18-JUL-1986; US-888033.
09-JUL-1990; US-550253.
14-AUG-1992; US-930970.
                                                                                                                                                                                                                                                          Inhibition of chitinous fungal plant pathogens - by transforming plant with DNA encoding chitinase activity
Disclosure; Fig.1; 13pp; English.
Plasmid pCHIT1251 containing the chitinase-A gene (chiA), fused directly to a nos promoter, may be used to transform, via Agrobacterium sp., a crop plant. The resulting transgenic plants expressing the chitinase-A protein fragment are protected against fungi, nematodes, insects and disease agents. The protein is preferably expressed by the plant only at the site of pathogen attack, e.g. only in the root cells. The plants express the chitinase in a biologically active form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R48981
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones JDG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial
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                              169
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  406
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DB; Q57966.
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alnar---pgsrhrlhhgegrecaagqgvkpgkivvgtamygrgwtgvngyqnnipftgt
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                            EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KVTGHNS
                                                    lwaetgr-kyeltsaisagkdkidkvaynvag--nsmdhiflmsydfygafdlknlghqt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1992; US-930970.
DNA PLANT TECHNOLOGY
                                                                                                                                                                                            Similarity
90; Conser
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                                                                                                                                                                                                                                                .g. only in the roc in a biologically 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Suslow T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iltinase-A fragment from pCHIT1251.
enzyme; transgenic plant; biological control;
stance; crop improvement; Agrobacterium; fungu
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                                                                                                                                                                                              Conservative
                                                                                                                                                                                                        10.9%;
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                                                                                                                                                                                           Score
Pred.
83; M
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.07e-22;
                                                                                                                                                                                            125;
                                                                                                                                                                                                                    Length
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                                                                                                                                                                                           Gaps
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Best Local S
Matches 5
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17-JUN-1993 (first entry)
2 HaNPY IE-1 gene protein (partial sequence).
4 Heliothis armigera nuclear polyhedrosis virus; Ha;
5 Heliothis armigera nuclear polyhedrosis virus.
6 Heliothis armigera nuclear polyhedrosis virus.
7 Heliothis armigera nuclear polyhedrosis virus.
8 Heliothis armigera nuclear polyhedrosis virus.
9 Heliothis armigera nuclear polyhedrosis virus.
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17 Heliothis armigera nuclear polyhedrosis virus.
18 Heliothis armigera nuclear polyhedrosis virus.
18 Heliothis armig
                                                                                                                                22-AUG-1996.
13-FEB-1996; U02332.
13-FEB-1995; US-386727.
(UYJO ) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Key
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Insect virus with reduced for controlling proliferat
N-PSDB; T36387.
Chitin biosynthetic enzymes
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                                                                                                                                                                                                                                                                                                   Vibrio furnissii.
WO9625424-Al.
                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1997 (first entry)
Periplasmic chitodextrinase,
Periplasmic chitodextrinase;
Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          л 15
WO2156 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 51pp; English.
The sequence is that encoded by the Heliothis armigera (Ha)
nuclear polyhedrosis virus (NPV) immediate early-1 (IE-1) g
                                                                                                                                                                                                                                                                                                                                                                     catabolism.
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Sequence 238 AA;
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DB; T36387.
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Similarity 34.1%;
58; Conservative
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chitin; oligosaccharide; catabolic;
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Pred. No. 1.95e-13;
43; Mismatches 51
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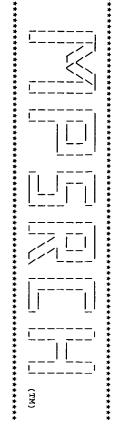
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Best Local :
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                                                                                                                                                                                                                                                                                periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:gluco:amidase(s), respectively Claim 2; Page 68-71; 101pp; English.

Periplasmic chitodextrinase (W02156), periplasmic Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02158) can be used to produce chitin oligosaccharides with the structure (GlcNac)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes endI, exoI and exoII respectively. They are all genes involved in the catabolic pathway of chitin.
                                                                                                                                                                                                                                                                         Sequence
   202
                                                                                                     491
                                                                                                                                                    550
                                                                     150
                                                                                                                                                                                            6.4%;
Local Similarity 31.1%;
les 52; Conservation
                                                                                                                                    94
                                                                                   LAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD-W--EYPGSQGSPA-
QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQ
                    qyLdyvnimsydlhgawndhvghnaalydtgkdselaqw-nvygtaq
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                                                                VD-KE-RETTLV---QDLANAFQQEAQ-TSGKE--RLLLSAAVPAGQTYVDAGYEVDKIA
                                                                                                                                                                                                                                                                         1046 AA;
                                                                                                                                                                                                 Score 220; DB 19; 19
Pred. No. 4.80e-09;
44; Mismatches 56;
                                                                                                                                                                                                                                   Length 1046;
                                                                                                                                                                                                   Indels 15;
 248
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Search completed: Fri Jun 27 16:59:22 1997 Job time: 98 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 27 16:56:14 1997; MasPar time 23.19 Seconds 572.791 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-663-618A-4 (1-466) from US08663618A.pep 3440 1 MYRSYAWAGEMYLLMIPWGS......QQSCPTGLYFSNSCKCCTWN 466

Scoring table: PAM 150 Gap 11

Searched: 89912 segs, 28507787 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir50

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 48.432; Variance 103.240; scale 0.469

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Length	- BB	Ŗ	Description		Pred. No
_	1513		- 1	13	A49562	cartilage g	lycoprote	9.27e-263
N	1456	42.3	383	16	13	arin	<u>ء</u> ٰ	. 65e-
ω	1453	٠		14	61	BRP39 protein		. 46
4	1453	•		14	I48271	BRP39 protein	•	. 466
ر.	1374	٠		Ç	S27879	secretory p	tei	• .
σ	1355	•		14	I46470	estrogen dependen	pendent o	
7	1339	٠		14	S57197	oviduct-speci	cific gly	1.85e-
æ	1179	•		12	A53918	chitinase (ω .2	4.64e-197
9	1080			12	A38221	_	3.2.	2
10	1025	29.8		12	A56596	ი 〜	EC 3.2.1.	5.30e-167
11	700	٠	699	10	A38368	е (~	EC 3.2.1.	
12	594		378	σ	S51591	chitinase (EC 3.2.1.	2.53e-84
13	585		424	₅	S47133	chitinase (EC 3.2.1.	
14	579		423	s	JQ1975	chitinase (EC 3.2.1.	1.66e-8
15	564		423	12	S51369	chitinase -	fungus (
16	548		427	12	JC4565	chitinase (EC 3.2.1.	1.04e-7
17	449		563	16	S60651	chitinase p	precursor	2.08e-5
18	407		561	9	A25090	Ø	EC 3.2.1.	.98e-
19	348		799	ထ	PC4106	е (~		.20e-
20	347	10.1	820	9	A40633	tinase (£C 3.2.1.	
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2.9	2.9	2.9	2.9	2.9	2.9	3.0	3.1	3.1	3.2	ω .ω	3.4	3.4	4.0	4.0	5.0	5.0	6.7	7.2	7.7	7.7	8.4	9.1	9.7
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alpha-glucosidase (E	serine proteinase (E	0	transporter protein	keratin, 56K type II	prote	probable membrane pr	retrovirus-related p	retrovirus-related c	(EC 3.	homologies with orf		chitinase (EC 3.2.1.	oviduct-specific sia	oviduct-specific gly	-stimula	39K whey protein - b	chitinase (EC 3.2.1.		RF2 protein - yeast	47K glycoprotein - f	chitinase (EC 3.2.1.	probable membrane pr	chitinase (EC 3.2.1.
	•		2.92e+00	2.25e+00		1.33e+00	7.78e-01	7.78e-01	1.98e-01	4.85e-02	2.73e-02	2.73e-02	8.90e-05	8.90e-05	6.14e-10	.14e-	.23e-	- '	4.99e-25	.99e-	.13e-	2.95e-33	.41e-

ALIGNMENTS

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			Query Match Best Local (Matches 2)	SUMMARY	1-21 22-3	## KEYWORDS FEATURE	# #		#	##	REFERENCE			Š	#	##	# #	REFERENCE		ORGANISM DATE	TITLE ALTERNATE_NAMES	RESULT
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Int	SAA	sау]		length 383	#do	lag	<pre>#cross-references MUID:90328983 #accession S10677 ##molecule_type protein</pre>	bovine period.	Human synovial cells secrete a	Nyirkos, P.; Golds, E.E. Biochem. J. (1990) 269:265-268	7 28	1-383 ##label	##molecule_type mRNA	preliminary	chondrocytes and synovial chitinase protein family.	ca:		A49562; S10677; A33162 A49562	03-мау-1996	#formal_name 23-Mar-1995	cartilage glycoprotein gp39 39K synovial protein	8
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skí	DPS	drf	Score 1513; DB 13; Pred. No. 9.27e-263; 89; Mismatches 83;	#molecular-weight 42613	#domain signal sequence #status #product cartilage glycoprotein	22-40,'X',42-45 ##label NY2 cartilage; extracellular protein; glycoprotein		bovine mammary protein expressed during period.	39 kDa protein						ß	ecr) (i)		:	#sequence revision 23-Mar-1995	precursor -	
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heparin-binding glycoprotein 38K - pig
#formal_name Sus scrofa domestica #common_name
07-May-1995 #sequence_revision 07-May-1995 #tex
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1-383 ##label
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383 #molecular-weight 42443
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Pred. No. 1.65e
88; Mismatches
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matches 94;
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             ##status preliminary; translated
##molecule_type mRNA
##residues_ 1-381 ##label RES
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1 Similarity 49.6%;
193; Conservation
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BRR93 protein - mouse
#formal_name Mus musculus #common_name house mouse
10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
03-May-1996
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BRR93 protein - mouse
fformal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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Oncogene (1994) 9:3417-3426
neu and ras initiate murine ma
markers generally absent in
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#length 381 #molecular-weight 43001
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89; Mismatches 96;
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CDS_PID: g1085066
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Similarity 49.6%;
193; Conservative
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Chang, N.C.A.;
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secretory protein rw-1 precursor - mouse
#formal_name Mus musculus #common_name house
17-Apr-1993 #sequence_revision 17-Apr-1993 #t
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Pred. No. 6.46e-251;
89; Mismatches 96;
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Pred. No. 2.39e-235;
95; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors DeSouza, M.M.; Murray, M.K.
#journal Endocrinology (1995) 136:2485-2496
#title An estrogen-dependent secretory protein, which shares identity with chitinases, is expressed in a temporally regionally specific manner in the sheep oviduct at the of fertilization and embryo development.
#cross-references MUID:95269691
#accession 146470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **status preliminary; translated from ##molecule_type mRNA
 356
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##cross-references EMBL:U16719; NID:g885600; CDS_PID:g885601
##cross-references EMBL:U16719; NID:g885600; CDS_PID:g885601
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tldlddfrgnfcgtgpfplahtlnnll
                             MLAYYEVCSW-KGATKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                  SLNVDAAVQQWLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGG
                                                                                                                                          LSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAA
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Similarity 48.6%;
188; Conservative
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estrogen dependent oviduct protein precursor -
#formal_name Ovis orientalis aries, Ovis ammon
#common_name domestic sheep
16-aug-1996 #sequence_revision 16-aug-1996 #tex
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Pred. No. 1.31e-231;
86; Mismatches 106;
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##status prel:
##molecule_type mRNA
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##residues 1-53
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#length 537 #checksum 1695
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                                                                                                                                                                                                                                                                                                                       38.98;
1 Similarity 50.18;
190; Conservation
  A53918
A53918
Krishnan, A.; Nair, P.N.; Jones, D.
Krishnan, A.; (1994) 269:20971-20976
J. Biol. Chem. (1994) 269:20971-20976
Isolation, cloning, and characterization of new chitinase isolation, cloning in chitin-lined venom reservoir.
                                                                                                                   A53918
chitinase
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#formal_name Bos primigenius taurus
28-Oct-1995 #sequence_revision 03-No
03-May-1996
                                                                                #formal_name Chelonus sp.
28-Jul-1995 #sequence_revision
03-May-1996
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S57197
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Biol. Reprod. (1994) 50:927-934
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                                                                                                                 #type complete
(EC 3.2.1.14) precursor -
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Pred. No. 1.85e-228;
81; Mismatches 101;
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glycoprotein 95K precursor
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chitinase in brugian #cross-references MUID:92179220
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RDS glycosidase; hydrolase
RY #length 483 #molecular-weight 52013
                                                                                                                                                                                                                                                                                                        ##status preliminary; not compared
##molecule_type nucleic acid; protein
##residues 1-504 ##label FUH
##rcross-references NCBIP:85345
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GSAAKLVCYFINWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLSTTE-WND--ET
avtklretnpglkvllsyggynfgsaiftgiaksagkterfiksaiaflrknnfdgfdld 146
|: || || || : || : : | : : |::||| ||| :||| EFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD 138
                                                                                                   NQGRYPLIQTLRQELS
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                                                                                                                                                          31.48;
1 Similarity 42.58;
157; Conservation
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l Similarity 42.0%;
158; Conservative
                                                                                                                                                                                                                                             sequence extracted from NCBI backbone
glycosidase; hydrolase
#length 504 #molecular-weight 55971 #che
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Transmission-blocking antibodies recognize microfilarial
chitinase in brugian lymphatic filariasis.
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04-Mar-1993 #sequence_revision
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Perler, F.B.
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Pred. No. 4.64e-197;
101; Mismatches 100;
                                                                                                                                                          Score 1080; DB 12;
Pred. No. 1.02e+177;
95; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                          161;
                                                                                                                                                                                                                                                                                                                                                                                                       h 29.8%; Score 1025; DB 12;
Similarity 38.5%; Pred. No. 5.30e-167;
161; Conservative 106; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kramer, K.J.; Corpuz, L.; Choi, H.K.; Muthukrishnan, S Insect Biochem. Mol. Biol. (1993) 23:691-701
Sequence of a cDNA and expression of the gene encoding epidermal and gut chitinases of Manduca sexta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycosidase; hydrolase
#length 554 #molecular-weight 62203
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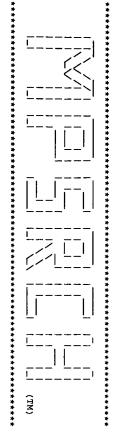
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-699 ##label WAT
##cross-references GB.J05599
FICATION #superfamily fibronectin type III repeat homology
IDS
glycosidase; hydrolase
y #length 699 #molecular-weight 73677 #checksum 6
##cross-references EMBL:X78325
            ##molecule_type mRNA
##residues 1-378 ##label HEI
                                                                                                                                                                                                                                                                                                                      309 W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL 360
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Similarity 40.4%;
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chitinase (EC 3.2.1.14) precursor - Bacillu
#formal_name Bacillus circulans
28-Jun-1991 #sequence_revision 28-Jun-1991
03-May-1996
                                                                                                                                                                                                         $51591 #type complete CC 3.2.1.17) PZ pathogenesis-related common tobacco pathogenesis-related common tobacco process related common page common.
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Gene cloning of chitinase Al from Bacillus circulans
revealed its evolutionary relationship to Serratia
chitinase and to the type III homology units of
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A38368
                                                                                   Heitz, T.; Segond, S.; Kauffmann, S.; Geoffroy
V.; Brunner, F.; Fritig, B.; Legrand, M.
Mol. Gen. Genet. (1994) 245:246-254
Molecular characterization of a novel tobacco
                                                                                                                                                    S51591; S51632; S43119
S51591
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                                                          pathogenesis-related
chitinase/lysozyme.
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Pred. No. 2.24e-104;
72; Mismatches 85;
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                                                                                                                                                                                                                                                              #description
                                                                                                                                                                                                                                                                           #submission
                                                                                                                                                                                                                                                                                                       #authors
                 112
                                                                                                                                                                                         ##molecule_type DNA
##residner
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##residues 31-36;8
                                                                                                                                                                         ##cross-references
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cession S51632
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qlfk-lkkanrnlkvmlsiggwtwst-nfpsaastdanrknfaktaitfmkdwgfdgidv 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDLDPSLCTHLIYAFAGMT--NHQLSTTEWNDETLYQEFNG-LKKMNPKLKTLLAI-GGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGS-W
                                           h 17.0%;
Similarity 36.4%;
103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 17.3%;
Similarity 32.7%;
106; Conservative
                                                                                                48/2; 81/2; 98/1
#superfamily Streptomyces chitinase chi40
glycosidase; hydrolase
#length 424 #molecular-weight 46298 #checksum
                                                                                                                                                                                                                                endochitinase gene
$47133
                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, June 1994 Characterization of ech-42, a Trichoderma har
                                                                                                                                                                                                                                                                                       S47133
S47133
Carsolio, C.; Gutierrez, A.; Jimenez, B.;
Herrera-Estrella, A.
                                                                                                                                                                                                                                                                                                                                                       $47133 #type complete chitinase (EC 3.2.1.14) - fungus (Trichoderma #formal_name Trichoderma harzianum 23-Nov-1994 #sequence_revision 03-Aug-1995 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycosidase; hydrolase
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                                                                                                                                                                         1-424 ##label CAR
es EMBL:X79381
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1 378 #molecular-weight 42019 #checksum
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Eamily Streptomyces chitinase chi40
                                         Score 585; DB 5; Leng
Pred. No. 1.24e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Samsun
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Pred. No. 2.53e-84;
87; Mismatches 108
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KEYWORDS
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SUMMARY
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#authors
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Best Local Similarity 36.6%;
Matches 102; Conservative
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##molecule_type mRNA
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##cross-references GB:X64104
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                                                                                                                                                                                                                          -adatqaqnmvlllqavrseldsyaaqy-akg-hhfilsiaapagpdnynklkfa-e-1g 228
                                                                                                                                                                                                                                                                                       | lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 173
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VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                  lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak 339
                                                                                                                                    QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI 261
                                                                                                                                                       GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA 201
                                                                                                                                                                                                                                                                        LKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 142
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                                                                  LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Aphanocladium album)
#formal_name Aphanocladium album
03-reb-1994 #sequence_revision 03
03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label #product chitinase 1 #status predicted #label MAY #length 423 #molecular-weight 46072 #checksum 8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily Streptomyces glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blaiseau, P.L.; Lafay, J.F.
Gene (1992) 120:243-248
Primary structure of a chitinase-encoding gene (chil) from
the filamentous fungus Aphanocladium album: Similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JQ1975
JQ1975
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ENTRY
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ORGANISM
Search completed: Fri Jun 27 16:57:26 1997 Job time : 72 secs.
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#title
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                                                                      169 dweyp-adatqasnmilllkevrsqrdayaaqy-apg-yhflltiaapagkdny-sklrl 224
                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary
##molecule_type DNA
##residues 1-423 ##label GAR
##residues 1-423 #molecular-weight 46056 #checksum 2000
                                                                                                                                               258 SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRI 317
                                                                                                                                                                    284 nkivlgmpiygrsf--qntag--igqtyngvgs-gsw--eagiwdykalpk-agatvqyd 335
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Sarcia, I.; Lora, J.M.; de la Cruz, J.; Benitez, T.; Llobell, A.; Pintor-Toro, J.A.
Curr. Genet. (1994) 27:83-89
Cloning and characterization of a chitinase (CHTT42) cDNA from the mycoparasitic fungus Trichoderma harzianum.
SS1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S51369 #type complete
chitinase - fungus (Trichoderma harzianum)
#formal_name Trichoderma harzianum
15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change
03-May-1996
S51360
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 27 16:54:21 1997; MasPar time 14.84 Seconds 666.076 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-663-618A-4 (1-466) from US08663618A.pep 3440 1 MVRSVAWAGFMVLLMIPWGS......QQSCPTGLVFSNSCKCCTWN 466

Scoring table: PAM 150 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 50.039; Variance 84.025; scale 0.596

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222111114 2220166 221066	Result No.
1513 1005 1025 700 570 544 440 398 394 394 304 290 290 172 172 172 172 172 172 172 172 172 172	Score
22344 22344 22344 2344 2344 244 244 244	Query Match Length
11111111111111111111111111111111111111	Length DB
GP39 HUMAN CHIT_BRUMAN CHIT_MANSS CHIT_MANSS CHIT_APHAI CHIT_APHAI CHIT_APHAI CHIT_COIN CHIT_STRUMAN CHIT_CHIT CHIT_STRUMAN CHIT_CHIT CHIT	!
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S 1.84e-213 S 1.84e-213 O 3.64e-132 O 3.64e-133 P 1.10e-96 O 6.62e-96 O 4.28e-61 O A 2.8e-61 O A 2.4e-30 O A 2.4e-30 O A 2.4e-30 O A 2.4e-31 O A 2.5e-10 O A 2.5e-10 O A 2.5e-10 O A 2.5e-10 O A 2.5e-10 O A 2.5e-10 O A 2.5e-10	Pred. No.

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YAJ1_SCHPO	GCH2_PICGU	YHO8_YEAST	EBAG_FLASP	Y150_NPVAC	COPI_DROME	VGR1_MOUSE	PRTS_SERMA	K2CF_HUMAN	K2CE_HUMAN	K2CC_HUMAN	K2CA_HUMAN	K2CB_HUMAN	HYES_MOUSE	HYES_RAT	SYK_THETH	UMUC_ECOLI	YQHT_BACSU	HMX1_HUMAN	AGLU_CANTS	PRTT_SERMA	AMYG_SCHOC	ひてにはしびこれでは
PUTATIVE FAMILY 31 GL	GTP CYCLOHYDROLASE II	HYPOTHETICAL 35.1 KD	ENDO-BETA-N-ACETYLGLU	HYPOTHETICAL 11.2 KD	COPIA PROTEIN.	VASCULAR ENDOTHELIAL	EXTRACELLULAR SERINE	TYPE II	Η	TYPE II	, TYPE II	KERATIN, TYPE II CYTO	SOLUBLE EPOXIDE HYDRO	SOLUBLE EPOXIDE HYDRO	LYSYL-TRNA SYNTHETASE	UMUC PROTEIN.	PUTATIVE PEPTIDASE IN	HOMEOBOX PROTEIN MSX-	ALPHA-GLUCOSIDASE PRE	EXTRACELLULAR SERINE	GLUCOAMYLASE 1 PRECUR	EVOLUNTIAL D EXECT
2.81e+00	2.81e+00	3.78e+00	3.78e+00	3.78e+00	2.08e+00	2.08e+00	8.30e-01	2.08e+00	2.08e+00	1.13e+00	1.13e+00	1.13e+00		1.54e+00	8.30e-01	8.30e-01	2.08e+00	1.54e+00	3.23e-01	.23e-	3e-	4.44E-01

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                                       Query Match
Best Local S
Matches 15
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01-DEC-1992 (REL. 2

01-DEC-1992 (REL. 2

01-FEB-1995 (REL. 3
                                                                               DOMAIN
DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                        CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE;
                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                   FUHRMAN J.A., LANI PROC. NATL. ACAD.
                                                                                                                                                                                                                                                                                                                                                                                     EUKARYÓTA; METAZOA; ACOELOMATES; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                         ENDOCHITINASE
                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                EMBL;
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                     27
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 26
                                                                                                                                                                                                                                                                                     C. NATL ACAD. SCI. U.S.A. 89:1548-1552(1992).
FUNCTION: THE MF1 ANTIGEN IS A MICROFILARIAL CHITINASE, FUNCTION TO DEGRADE CHITIN-CONTAINING STRUCTURES IN THE FILARIA OR IN ITS MOSQUITO VECTOR DURING PARASITE DEVELOPMENT
                                                                                                                                     ; M73689; 38221.
A38221; A38221.
SITE; PS01095; CHITINASE_18.
ROLASE; GLYCOSIDASE; CHITIN DEGRADATION;
ROLASE: "COROTEIN; CALCIUM-BINDING.
                                                                                                                                                                                                                KNOWN TO BIND CALCIUM.

DEVELOPMENTAL STAGE: THE APPEARANCE OF THE ME1 ANTIGEN CORRESPOND WITH THE ONSET OF THE PARASITE'S ABILITY TO INFECT THE MOSQUITO. SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: HYI
N-ACETYL-D-GLUCOSAMINE
                                                                                                                                                                                                                                                            PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                          HYDROLASES)
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         gymlrlgapasklvmgiptfgrsftlass-etgvgapisgpgipgrftkeagtlayyeic
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                                         l Similarity
157; Conse
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                                                                              23
23
401
407
148
504
                                      31.4%;
larity 42.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        PRECURSOR (EC
                                                                                AA;
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                                                                          22
504
400
450
448
148
155971
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24, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
CURSOR (EC 3.2.1.14) (MF1 ANTIGEN).
                                                                                                                                                                                                                                                                              HYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE.
                                                                                Œ;
                                                                                                                                                                                                                                                                      POLYMERS
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                                       Score
Pred.
95; M
                                                                           CATALYTIC.
SER/TH-RICH (LINKER).
3 X 14 AA APPROXIMATE TANDEM
PROTON DONOR (BY SIMILARITY).
4 DA7E5EB CRC32;
                                                                                                                                  ENDOCHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                      re 1080; DB 2; I
l. No. 4.93e-225;
Mismatches 102;
                                                                                                                                                                                                                                                                     OF THE BETA-1,4
S OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            504
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                                                           Length
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                                                            504;
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MICRO
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-LYQ
                                      Gaps
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CARBOHYD
SEQUENCE
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01-JUN-1994
01-FEB-1995
                                                                                                                 HYDROLASE;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; LEPIDOPTERA.
                                                                                                                                                 PROSITE;
                                                                                                                                                                                                    +++
                                                                                                                                                                                                                                                                                                 <del>'</del>
                                                                                                                                                                                                                                                                                                                   KRAMER K.J., CORPUZ L., CHOI
INSECT BIOCHEM. MOL. BIOL. 2
-!- FUNCTION: DIGEST CHITIN
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 93357793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                P36362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIT_MANSE
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          Local
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                                                                                                                                                                                                                    CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH PRAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LCUPLES SEEN ON DAYS 0, 7 AND 8.

TISSUE SPECIFICITY: EPIDERMIS AND GUT.
                                                                                                                                                                                                   SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                          HYDROLASES)
                                                                                                                                                                                                                                                                                                           PROCESS
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 ch 29.8%;
l Similarity 38.5%;
161; Conservative
                                                                                                                                                  PS01095;
                                                   ; GLYCOSIDASE;
1 19
20 554
396 453
146 146
85 85
85 85
303 303
407 407
545 545
                                          396
146
85
303
407
545
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                                                                                                                                                                   NOT_ANNOTATED_CDS
                                                                                                                                     CHITINASE_18.
IDASE; CHITIN DEGRADATION;
                                           62203
                                                                                                                                                                                                                                                                                                                  CHOI H.K., MUTHUKRISHNAN OL. 23:691-701(1993).
                                                                                                                                                                                                    OT
                                          MW.
                                                                                                                                                                                                              SECRETED
  106;
                                                                                                                                                                                                    CHITINASE
          Score 1025; DB 2;
Pred. No. 1.84e-21
                                                   PROTON DONOR POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.
                                                                                                      ENDOCHITINASE.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                          FA87F8AD
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           554
                                         CRC32;
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  126;
                                                                                                                                      SIGNAL;
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                    Length
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  25;
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Gaps
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Query Match
Best Local
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MEDLINE; 93366760.
WATANABE T., KOHORI K
UCHIDA M., TANAKA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P20533;
01-FEB-1991
01-FEB-1991
01-FEB-1995
                                                                      ACT_SITE
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
WATANABE
                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                J. BIOL. CHEM. 268:18567-18572(1993).

-I- CATALYTIC ACTIVITY: HUDROLYSIS OF THE BETA-1,4 LINKAGES ON ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS CIRCULANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHITINASE A1
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                                                                                                                                                                                                                                                                                        PIR; A38368; A38368.
HSSP; P07254; 1CTN.
                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS
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                                                                                                                                                                                                                                                      YDROLASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL.
                                                                                                                                                                                                                                                                                                                                                    HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLDDFAGFSCNQGRYPLIQTLRQELSLPY-LPSGTPELEVPKPGQPSEPEHGPSPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QWLQKGTPASKLILGMPTYGRSFTLASSSDT-RVGA--P-ATGSGTPGPFTKEGGMLAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frlmegyhvpelcqeldaihvmsydlrgnwagfadvhsplykrphdqwayeklnvndglh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFDGLDLDWEYPGS--QGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dfdgldldweypgaadrggsfsdkdkflylvgelrraf---irv-gkgwel-taavplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-DETLYQEFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90368776.
T., SUZUKI K., OYANAGI W., CHEM. 265:15659-15665(1990)
                                                                                                                                                                                                                                                                            PS01095;
                                                                                                                                                                                                                                                      GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOHORI K., MIYASHITA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR
                                                                                                                                                                                                                                                                                                                                G142688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17,
17,
31,
                                                                                                                                                                                                                                                CHITINASE_18.
IDASE; CHITIN DEGRADATION;
                                                                            544
544
204
200
200
200
20.3%;
                                                            73677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENT LAST ANNOTATION (EC 3.2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE UPDATE)
ANNOTATION UPDAT
3.2.1.14).
                                                                      CHITINASE A1.

CAPALYTIC.

FIBRONECTIN TYPE-III (R-1).

FIBRONECTIN TYPE-III (R-2).

PROTON DONOR (PROBABLE).

D-N: DECREASE IN ACTIVITY.

D-SE: NO CHANGE IN ACTIVITY.

E-D,Q: LOSS OF ACTIVITY.
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
No.
                700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OHNISHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         699
; DB 2; L
3.64e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUJII T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UPDATE)
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                                                                                                                                                                                                                                                    SIGNAL;
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                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAKAI H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCCI;
                                                                                                                                                                                                                                                      REPEAT
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                                                                                                       Matches
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993
01-FEB-1996
01-FEB-1996
                                                                                                                                               CHAIN
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                     MEDLINE; 92136437.
BLAISEAU P.-L., KUNZ C., GRISON CURR. GENET. 21:61-66(1992).
                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93013040.
BLAISEAU P.-L., LAFAY J
GENE 120:243-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIL_APHAL P32470;
                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: HYDROLYSIS OF THE N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHI
                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 35-57.
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ETHM 483
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                APHANOCLADIUM ALBUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHITINASE 1
                                                                                                                                                                               PROPEP
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                     PIR; JQ1975; JQ1975.
HSSP; P07254; 1CTN.
                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS
                       143
                                                                          115 lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
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                                          174
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   229
                                                              83
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                                                                                                                  Local
                                                                                                                                                                                                                                                     HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ntelakiaaivdwinimtydfngawqkisahnaplnydpaasaagvpdantfnvaagagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv
                                       -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-lg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yinkngytrywndtakvpylynasnkrfisyddaesvgyktayikskglggamfwel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hldagvpaaklvlgvpfygrgwd-gcaqagn-gqyqtctggssvgtweagsfdfydlean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPL-YKRQE-ESGAA-A-SLNVDAAVQQ 249
                     GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG
                                                             LKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEV-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD
                                                                                                                                                                                                                                         X64104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120;
                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                ETYL-D-GLUCOSAMINE POLYMERS
                                                                                                                                                                                                            PS01095;
                                                                                                                                             171
423
                                                                                                                                                                                                    GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                        Conservative
                                                                                                                                                                                                                                          G429026;
                                                                                                                                                AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                27, CREATED)
33, LAST SEQUENCE UPDATE)
33, LAST ANNOTATION UPDAT
RSOR (EC 3.2.1.14).
                                                                                                                                                                                                            CHITINASE_18.
                                                                                                                                                                                                                                                                                                                                                                                                                      DEUTEROMYCOTINA (IMPERFECT FUNGI).
                                                                                                                 16.8%;
                                                                                                                                                46058
                                                                                                                                                                                                  CHITIN DEGRADATION;
                                                                                                                                                ¥;
                                                                                                      Score
Pred.
64; M
                                                                                                                                              POTENTIAL.

POTENTIAL.

CHITINASE 1.

PROTON DONOR (BY S

#; 88456E6E CRC32;
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                                                                                                       Mismatches
                                                                                                                 579; DB 2; I
No. 3.08e-103;
                                                                                                                                                                                                                                                                                                               BERTHEAU Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
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                                                                                                                                                                                                                                                              ΙΙ
                                                                                                                                                                                                  SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                               (FAMILY
                                                                                                                        Length
                                                                                                                                                                                                                                                                                                               BRYGOO
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                     -QTYVDAGYEVDKIA
                                                                                                                                                                                                                                                                                            LINKAGES
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                                                                                                      18;
                                                                                                                                                                                                                                                               OF GLYCOSYL
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                                                                                                                                                                                                                                                                                            QF
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                                                                                                      Gaps
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                                                              142
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 287
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RESULT 6

RESULT 6

ID CHI4_TRIHA
AC P48827;
DT 01-FEB-1996 6
DT 01-FEB-1996 6
DT 01-FEB-1996 6
DE 42 KD ENDOCHI
GN CHIT42.
OS TRICHODERMA FOR EUKARYOTA; FU
RN [1]

RP SEQUENCE FROM
RX MEDLINE; 952K
RA GARCIA I. L.
RA PILNOR-TORO 1.
CC -1- FUNCTION 1.
CC -1- FUNCTION 1.
CC -1- FUNCTION 1.
CC -1- SUBCELLUI
CC -1- SUBCELUI
CC -1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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Best Local S
Matches 10
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-I-CATALYTIC ACTIVITY: HYDROLYSIS C
N-ACETYL-D-GLUCOSAMINE POLYMERS
-I- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PINTOR-TORO J.A.;
CURR. GENET. 27:83-89(1994).
-!- FUNCTION: MORPHOGENETIC ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE MEDLINE; 95269313.
GARCIA I., LORA J.M., LA CRUZ J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHITIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S78423;
HYDROLASE; GL!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                 138
                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                             322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
   318
                                                                            258
                                                                                                                284
                                                                                                                                                      198
                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: SPECIFICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   svakgyysynsatkelisfdtpdmintkvaylkslglggsmfw
                                                                                                                                                                                                                           QDQKVPYIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                            adlgqvldyinlmaydyagsfspltghdanlfnnpsnpnatp-fntdsavkdyinggvpa
                                                                                                                                                                                                                                                                                                          QEFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRI
                                                                                                                                                    DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-1996 (REL. 33, CREATED)
B-1996 (REL. 33, LAST SEQUENCE UP
B-1996 (REL. 33, LAST ANOTATION
ENDOCHITINASE PRECURSOR (EC 3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTION: MORPHOGENETIC ROLE DURING APICAL GROWTH, CELL DIVISION DIFFERENTIATION (CELL WALL MORPHOGENESIS). ANTIFUNGAL
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
23
35
171
171
218
423 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNGI;
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FUNGI; DEUTEROMYCOTINA
                                                                                                                                                                                                                                                                                                                                                                                 16.4%;
larity 36.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G999376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
34
423
171
218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                42 KD ENDOCHITLNASE
PROTON DONOR (BY SI
POTENTIAL.
W; 899DA50A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                 Score 564; DB 2;
Pred. No. 1.10e-99,
70; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KD ENDOCHITINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35-52;
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                                                                                                                                                                                                                                                                                                                                                                                   94;
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RESULT 7

RESULT 7

RESULT 7

RESULT 11

AC P54196;

DT 01-0CT-1996

DT 01-0CT-1996

DT 01-0CT-1996

DT 01-0CT-1996

DE ENDOCHITINAS

DE (CF-ANTIGEN)

GN CTS1.

OS COCCIDIOLDE;

OC EUKARYOTA;

RN [1]

RP SEQUENCE FR

SEQUENCE FR

MEDLINE; 96;

RA PISHKO E.J..

RA PISHKO E.J.

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Best Local :
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EMBL; U51271; G1256769;
EMBL; U32265; G1255728;
HYDROLASE; GLYCOSIDASE;
GLYCOPROTEIN.
                  CHIA_SERMA
P07254;
01-APR-1988
01-FEB-1995
01-FEB-1995
CHITINASE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P54196;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (COMPLEMENT-FIXATION (CF-ANTIGEN) (CF-AG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SILVEIRA;
YANG C., ZHU Y., MAGEE D.M.,
SUBMITTED (MAR-1996) TO EMBL,
-!- CATALYTIC ACTIVITY: HYDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96144270.
PISHKO E.J., KIRKLAND T
GENE 167:173-177(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCCIDIOIDES IMMITIS EUKARYOTA; FUNGI; DEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 lkknnrnlktllsiggwtysp-nfktpasteegrkkfadtslklmkdlgfdgididweyp
                                                                                                                                                                                                                                                                                 340
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QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
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                                                                                                                                                                                                                                                                                                                         LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
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EMBL/GENBANK/DDBJ DATA BANKS.
HYDROLYSIS OF THE BETA-1,4 LINKAGES
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ENDOCHITINASE 1.
POTENTIAL.
RWLSLECLECELGREMETLSTVTAVTVVTDDIQ ->
RWLSLECLECELGREMETLSTVTAVTVVTDDIQ ->
SMSSMPNYPVPEAPEGGFRSVVYFVNW (IN RE)
K -> N (IN REF. 2).
MW; 6CB9AF73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 548; DB 2;
Pred. No. 6.62e-96;
70; Mismatches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
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SERRATIA MARCESCENS

(REL. 07, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
PRECURSOR (EC 3.2.1.14).

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE 2:1169-1180(1994).
-!- CATALYTIC ACTIVITY: HYDR
N-ACETYL-D-GLUCOSAMINE P
-!- SIMILARITY: BELONGS TO C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. KOO J.C., LIM C.O., CHO M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
MEDLINE; 95219379.
PERRAKIS A., TEWS I., DAUTER Z., OPPENHEIM A.B., CHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
JONES J.D.G., GRADY K.L.,
EMBO J. 5:467-473(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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                                       523
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; X03657; G46831;
A25090; A25090.
                                                                                                                                                                                                                                                                                                  TKVSYLKQKGLGGAMVWALDLDD
                                     akgkyvldkglgglfsweidadn
                                                                                                   AFAGMTNHQLSTTEWNDE-T-LYQEFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATAN
                                                                           GSGTPGPFTKEGGMLAYYEVCS-WKGATKQ
                                                                                                                                                 PLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPAT
                                                                                                                                                                                                                            EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KVTGHNS
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P07254; 1CTN.
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94; Conser
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larity 29.1%;
Conservative
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IDASE; CHITIN
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60979
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430
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467
473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLYSIS OF THE BETA-1,4 LINKAGES INE POLYMERS OF CHITIN.
TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TA -> GP (IN REF. 2).
A -> P (IN REF. 2).
V -> I (IN REF. 1 AND 2).
P -> A (IN REF. 1 AND 2).
PAWKRDTAYTTVNGYWALLAQ -> RE
AAGQ (IN REF. 1 AND 2).
V -> I (IN REF. 2).
V -> I (IN REF. 2).
ATGP -> HRA (IN REF. 2).
K -> E (IN REF. 2).
K -> E (IN REF. 2).
G -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 440; DB 2; L4
Pred. No. 1.04e-70;
83; M1smatches 123;
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364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIM C.Y.,
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                                                                           -RIQD-QKVPYIFR-DN-QWVGFDDVESFK
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Best Local S
Matches 9
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P32823;
01-OCT-1993
01-OCT-1993
01-FEB-1995
CHITINASE A
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SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 943U31...

AYRES M.D., HOWARD S.C., KUZLU U., AYRES M.D., HOWARD S.C., KUZLU U., AYRES M.D., HOWARD S.C., KUZLU U., AYRES M.D., HOWARD S.C., KUZLU U., AYRES M. ACTIVITY: HYDROLYSIS OF THE BIN-ACETYL-D-GLICOSAMINE POLYMERS OF CHIT N-ACETYL-D-GLICOSAMINE POLYMERS OF CHIT NASE CLASS
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SIGNAL
CHAIN
ACT_SITE
CARBOHYD
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS
VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE;
                                                                                 CHIA.
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PROSITE; PS0109
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01-NOV-1995
VIBRONACEAE [1]
                                        ALTEROMONAS PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIT_NPVAC
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96; Conser
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173
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551 ?
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                                                                                           (REL. 27, CREATED)
(REL. 27, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
PRECURSOR (EC 3.2.1.14) (CHI-A).
                                        SP. (STRAIN O GRACILICUTES;
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larity 29.5%;
Conservative
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                                                       (STRAIN 0-7)
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CHITINASE_18.
IDASE; CHITIN DEGRADATION; SIGNAL;
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                                        SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
79; M
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                                                                                                                                                                                                      PRT;
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1. No. 4.28e-61;
Mismatches 122
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LASS II
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                                        FACULTATIVELY
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EUBACULOVIRINAE.
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                                        ANAEROBIC
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Best Local
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TSUJIBO H., YOSHIDA CAN. J. MICROBIOL.
                                                                                                                                                                                                                                                                      CHIB_SERMA
P11797;
01-OCT-1989
01-OCT-1989
01-FEB-1995
CHITINASE B
                                                                                                                                                                                                       SERRATIA MARCESCENS.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
ACT_SITE
SEQUENCE
 EMBL;
PIR; (
                                               SEQUENCE FROM N.A. STRAIN-ATCC 990 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSUJIBO H., ORIKOSHI H., TANNO H., IMADA C., OKAMI Y., INAMORI Y.; J. BACTERIOL. 175:176-181(1993).
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BL; D13762; G216207; -.
BL; D13762; G216207; -.
SP; P07254; ICTN.
OSITE; PS01095; CHITINASI
DROLASE; GLYCOSIDASE; CH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
ENZYME REGULATION: STIMULATED BY MG2+; INHIBITED BY
N-BROMOSUCCINIMUDE AND 2-HYDROXY-5-NITROBENZYL BROMIDE
SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE OPTIMUM PH AND CELSIUS, RESPECTIVE
               HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S04856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYQEFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYSF-DG
                                                                                                                                                                                                                                                                                                                                                                                                                            -QTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ydkiedvdygaag--gymdyifamtydfygawnnetghqtgiy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ.,
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22
313
820
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larity 35.6%;
Conservative
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                 Ġ47228;
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                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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IDASE; CHITIN DEGRADATION;
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820
313
87346
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(EC 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMADA C.,
                                                                                                                                                                                                                                                                      r SEQUENCE UPDATE) RANNOTATION UPDAT 3.2.1.14).
                                                                                                                                                                                                                       SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 348;
Pred. No. 7.
43; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHITINASE A.
PROTON DONOR (BY
838F6EE8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57:1396-1397(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                             499
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7.81e-50;
tches 47;
                                                                                                                                                                                                                       FACULTATIVELY ANAEROBIC RODS
                                                                                                                                                                                                                                                                                                                                                           B
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C.,
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                                                   GLYCOSYL
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RESULTATION OF THE PROPERTY OF
                                                                                                                                                                                                     HSSP; PO7254; 1CTN.

PROSITE; PS00018; EF_HAND.

R PROSITE; PS00051; CBD_BACTERIAL.

R PROSITE; PS01095; CHITINASE_18

W HYDROLASE; CHOOSIDASE; CHITIN DEGRADATION; CHITIN-BIND FT SIGNAL 1 30 CHITINASE C.
FT CHAIN 31 619 CHITINASE C.
FT CHAIN 35 140 CELLULOSE-BINDING.
FT DOMAIN 35 140 CELLULOSE-BINDING.
FT DOMAIN 148 230 EIBRONECTIN TYPE-III.
FT DOMAIN 240 619 CATALVIIC.
FT DOMAIN 382 PROTON DONOR (BY SIMILA)

CTONO MW; 23E3E1EC CRC32;
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Best Local S
Matches 5
                                                                                                                                                        Query Match
Best Local S
Matches 8
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01-JUN-1994
01-JUN-1994
01-FEB-1995
CHITINASE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
ACT_SITE
SEQUENCE
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J. GEN. MICROBIOL. 139:677-686(1993).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIT_STRLI
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  128
                                         369
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OSITE; PS01095; CHITINASE_18.
DROLASE; GLYCOSIDASE; CHITIN DEGRADATION; STEENAL
1 41 CHITINASE B.
42 499 PROTON DONOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                              71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-ACETYL-D-GLUCOSAMINE INDUCTION: BY CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASES).
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                        rwadvfdgidldweypnacglscdetsapnafssmmkamraefgqdylita-a---vtad
RKYS-FDGLDLDWEYPGSQG-S--PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAA
                                                                                                                                                        h 8.8%;
Similarity 28.5%;
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
53; Conser
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(REL. 29,
(REL. 31,
PRECURSOR
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LAST SEQ
LAST ANN
(EC 3.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE III-LIKE DOMAIN BACTERIAL-TYPE CELLULOSE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHITINASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYMERS
                                                                                                                                                        Score 304;
Pred. No. 3.
64; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2.1.14).
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Pred. No. 1.68e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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ON UPDATE)
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F CHITIN.
                                                                                                                                                        DB 2; Le
3.91e-40;
tches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREPTOMYCETACEAE
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                                                                                                                                                                                                                                                          SIMILARITY).
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RESULT COMPANY OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
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                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M82804; G153216; ...
EMBL; M82804; G153209; ...
EMBL; M18397; G153209; ...
PIR; A29912; A29912.
PIR; JH0573; JH0573.
HSSP; P07254; LCTN.
                                                                                                                                                                                                 DOMAIN
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROBBINS P.W., ALBRIGHT C., BENFIELD J. BIOL. CHEM. 263:443-447(1988).
-!- CATALYTIC ACTIVITY: HYDROLYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 13
CHIT_STRPL
P11220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 92192480.
ROBBINS P.W., OVERBYE
GENE 111:69-76(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (REL.
01-DEC-1992 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-45 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOMYCES PLICATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHITINASE 63
                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
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                                         77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CBD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASES).
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dldweypnacglscdetsapnafssmmkamraefgqdylita-a---vtadgsdggk-id
                                       YQEFNGLKKMNPKLKTLLAIGGWNFSTQKFTDMVATANNRQTFVNSAIRFLRKYS-FDGL
                                                                         fnqlrnlkaeyphikilysfggwtwsgg-fpdavknpaafakschdlvedprwadvfdgi
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                                                                                                                   n 8.4%;
Similarity 26.7%;
79; Conservative
                                                                                                                                                                                                                                                                                                                                                         PS00018; EF_HAND.
PS000561; CBD_BACTERIAL.
PS01095; CHITIMSE_18.
E; GLYCOSIDASE; CHITIN DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88087127
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148
236
383
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31,
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140
229
610
383
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LAST SEQUENCE UP
LAST ANNOTATION (
CC 3.2.1.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHITINASE CLASS II (FAMILY
                                                                                                                                                                                                 CHITINASE 63.
CELLULOSSE-BINDING.
FIBRONECTIN TYPE-III.
CATALYTIC.
PROTON DONOR (BY SIMILARITY).
F -> I (IN REF. 2).
M; 2F5E8E35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND SEQUENCE
                                                                                                                   Score 290; DB 2;
Pred. No. 4.24e-37;
62; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                             CHITIN-BINDING; SIGNAL
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                                                                                                                                                            Length
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                                                                                                                   Gaps
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          -!- SIMILARITY: LOCAL, TO
-!- SIMILARITY: BELONGS T
EMBL; X07127; G2829; -
EMBL; X00762; G2844; -
EMBL; X01095; G2849; -
PIR; S07915, S07915.
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
MEDLINE;
TOKUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CBS 2359/152;
SOR F., FUKUHARA H.;
CURR. GENET. 9:147-155(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
KILLER TOXIN ALPHA AND BETA SUBUNITS PRECURSO
(ENDOCHITINASE (EC 3.2.1.14)).
                                                                                                                                                                                  CHITINASE ACTIVITY OF ALPHA-SUBUNIT.
MEDLINE; 91301161.
BUTLER A.R., O'DONNEL R.W., MARTIN V.J., GOODAY G.W.,
EUR. J. BIOCHEM. 199:483-488(1991).
                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF MEDLINE; 87004569 STARK M.J.R., BOYI
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 84297209.
STARK M.J.R., MILE
NUCLEIC ACIDS RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P09805;
01-MAR-1989
                                                                                                                                                                                                                                                         MEDLINE; 90259069.
BRADSHAW H.D. JR.;
                                                                                                                                                                                                                                                                               SIMILARITY TO CHITINASE
                                                                                                                                                                                                                                                                                                        EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLUYVEROMYCES LACTIS (YEAST). PLASMID PGKL-1.
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
                                                                                                   THE BETA SUBUNIT IS A POTENT EXOCHITINASE. ALONG WITH ENERTH SUBUNIT IT PLAYS A ROLE IN THE INITIAL INTERACTION OF THE TOXIN WITH SENSITIVE CELLS AND ALLOW THE GAMMA SUBUNIT (THE ACTIVE TOXIN) TO GAIN ENTRY INTO THE CELL.

PTM: RF2 IS POTENTIALLY SPLIT BY MEMBRANE-BOUND BASIC AMINO ACID-SPECIFIC PEPTIDASE TO YIELD THE ALPHA AND BETA SUBUNITS: ALPHA, SUBUNIT: THE KILLER TOXIN IS COMPOSED OF THREE SUBUNITS: ALPHA,
                                                                                           BETA AND GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATKORIODOKVPYIFRDNOWVGFDDVESFKTKVSYLKOKGLGGAMVWALDLDDFAG
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                                                                                                                                                                                                                                                                                                      5:1995-2002(1986).
PS00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNGI;
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                                                                                                                                                                                                                                                                                                                   BOYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
CHITIN_BINDING
                                                                                                                                                                                                                                                                                                                                        PROTEIN,
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                                                                                                                                                                                                                                                                                                                    Α.;
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LAST SEQUENCE UPDATE)
                                                                    S TO
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                                                                  OTHER CHITIN-BINDING PI
O FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                               ALPHA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ROMANOS M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN)
                                                                                                                                                                                                STARK
                                                                                                                                                                                                M.J.R.;
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Best Local S
Matches
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P30922;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CARTILAGE GLYCOPROTEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGME)
BOS TAURUS (BOVINE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
CHAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
CARBOHYD
                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                 SEQUENCE.

MEDLINE; 88106603.

REJMAN J.J., HURLEY W.L.;

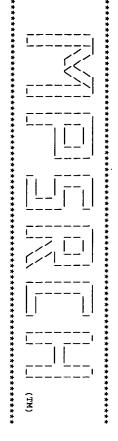
BIOCHEM. BIOPHYS. RES. COMMUN. 150:329-334(1988).

-I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE CAPACITY RESPOND TO AND COPE WITH CHANGES IN THEIR ENVIRONMENT-

-I- PIM: GLYCOSYLATED.
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248 QQWLQK-GTPASKLILGMPTYGRSFTLASSS 277
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                                                                                                                                                                                                                          TISSUE SPECIFICITY: MAMMARY SECRETIONS COLLECTED DURING MONLACTATING PERIOD.
SUBCELLULAR LOCATION: EXTRACELLULAR.
SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
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klixyytswsqyregdgsxfpda1dpf1xthv1ys
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                                                              h 5.0%;
Similarity 48.6%;
17; Conservative
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Similarity 28.9%;
61; Conservative
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26, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
0TEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGMENT).
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4264 MW;
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                                                            Score 172; DB 4; Le
Pred. No. 4.73e-13;
11; Mismatches 7;
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Pred. No. 5.77e-32;
57; Mismatches 74;
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BETA SUBUNIT (PROBABLE).
CHITIN-BINDING (BY SIMILA
                                                                                                                                            F3935740 CRC32;
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ALPHA SUBUNIT
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                                                                                                  Length 36;
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Qy 23 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYA 57

Search completed: Fri Jun 27 16:55:57 1997 Job time: 96 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 27 17:03:11 1997; MasPar time 9.60 Seconds 423.242 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

>US-08-663-618A-14
(1-373) from US08663618A.pep
2721
1 AKLVCYFINWAQYRQGEARF.....YPLIQTLRQELSLPYLPSGT 373

Scoring table: PAM 150 Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 34.970; Variance 153.103; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
200	t score
1328 1303 1303 1303 881 597 5897 576 576 576 576 576 99	•
48.8 47.9 447.9 221.9 221.9 221.2 21.2 21.2 21.2 21.3 21.4 21.3 21.3 21.3 21.3 21.3 21.3 21.3 21.3	Query Match
537 668 7188 321 371 371 377 389 424 424 424 1046 561 561 561 561 561 561 561 561 561 56	Length
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R73991 R73993 R73992 R73992 R70025 R70029 R63441 R56861 R33072 R33078 R330778 R33078 R33078 R33078 R33078 R33078 R33078 R33078 R33078 R330778 R3507	Ħ
Bovine oviduct specif Hamster oviduct specif Murine oviduct specif Murine oviduct specif Polypeptide involved Tobacco cluster-A pro Trichoderma harzianum Aphanocladium album m Aphanocladium album m Aphanocladium album m Soluble chitinase. Chitinase A. Bacterial chitinase. Batterial chitinase A. Batterial chitinase A. Batterial chitinase A. Batterial chitinase A. Batterial Schitlinase A. Batterial Schitlinase A. Batterial Schitlinase A. Batterial Chitinase A. Batterial Schitlinase A. Batteria	Description
7.85e-114 2.08e-1111 9.90e-71 9.86e-44 9.86e-44 9.86e-44 3.16e-42 9.31e-42 9.31e-42 9.31e-42 1.32e-31 3.32e-31 3.32e-31 3.32e-31 7.79e-23 9.19e-14 3.07e-09 1.21e-02 2.08e-02	Pred. No.

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R78223	P50059	P50319	R43257	R92750	R90772	R36735	R32904	R07311	R47264	R98125	P50017	P70423	P50018	R88058	R97235	R70746	R70752	R26999	R47259	R07575	P81181	R80445	R31372	R86905
Human Factor-VIII:c.	Human factor VIII.	Human antihaemophilic	Human Factor VIII.	Human EGF receptor su	Bacillus stearothermo	Human BMP-6.	Human BMP-6 peptide s	Human Bone Morphogene	Pre-pro BMP6.	mphocyte	Sequence encoded by t	FixD nitrogen fixatio	Sequence encoded by t	Protein encdoed by Mu	MuTu putative oncogen		YKL-40 internal pepti	Novel type III RTK en	Pre-pro-VGR1.	Glucoamylase encoded	Sequence of glucoamyl	Murine soluble epoxid	Murine bone morphogen	Murine BMP-9.
9.04e+01	9.04e+01	7.76e+01		6.65e+01	7.76e+01	6.65e+01	6.65e+01	6.65e+01	6.65e+01	7.76e+01	4.88e+01	4.88e+01	4.88e+01	4.88e+01	4.88e+01	4.18e+01	4.18e+01	3.57e+01	٠	1.17e+01	•	1.17e+01	1.17e+01	1.17e+01

ALIGNMENTS

Qy 121 PGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIA 180	_
Db 140 pglrgspardrwtfvflleellqafkneaqltmrprlllsaavsgdphvvqkayearllg 199	
Qy 61 GLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEY 120	_
Db 80 klkernrglktllsiggwnfgtvrfftmlstfsnrerfvssviallrthgfdgldlffly 139	
Qy 2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLSTTEWNDET-LYQEFN 60	_
Db 20 klvcyftnwafsrpgpasilprdldpflcthlvfafasmsnnqivpkdpqdekilypefn 79	
Matches 187; Conservative 74; Mismatches 97; Indels 7; Gaps	
SQ Sequence 537 AA;	
BOGP in high quantities.	_
PS Claim 4; Pages 7-9; 22pp; Japanese.	
recombinant protein production in high culantities	
DR · N-PSDB; Q90442.	
17.107979-1	
Peptide	
sig_pept	
Peptide	
Key	
	_
BOGP.	
KW Boying oviduat specific glycoprotein: recombinant production:	
DT 10-JAN-1996 (first entry)	
AC R73991;	
ID R73991 standard; Protein; 537 AA.	
RESULT 1	

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recombinant production;

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Best Loc
Matches
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/label mat peptide
J07107979-A.
25-APR-1995.
15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO KK
WPI; 95-190179/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q90444.

New DNA encoding an oviduct-specific glycoprotein - useful frecombinant protein production in high quantities.

Claim 4; Pages 16-18; 22pp; Japanese.
Q90444 encodes R73993 hamster oviduct specific glycoprotein The CDNA can be used for the commercial recombinant prodn. on Boursel of the CDNA can be used for the commercial recombinant prodn. on Boursel of the commercial recombinant prodn.
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N-PSDB;
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                                        AQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKL
                                                                                                                                                                                                                       grrldfinvlsydlhgswekstghnsplfslpedpkssa-famn--y--wrnlgapadkl
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l Similarity 48.4%;
177; Conservative
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No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
2.08e-111;
cches 99;
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding an oviduct-specific glycoprotein - useful recombinant protein production in high quantities. Claim 4; Pages 11-14; 22pp; Japanese. 090443 encodes R73992 murine oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. MOGP in high quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
/label=
Peptide
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J07107979-
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Murine oviduct specific glycoprotein.
Murine oviduct specific glycoprotein;
Immune response; J63032898-A.
                  P81342;
19-OCT-1990 (first entry)
Polypeptide involved in promine response; cell grow
                                                                                                          T 4
P81342 standard;
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R73992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1994; 214227.
19-AUG-1993; JP-227881
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                                                                                                                                                                                                                                                                                                         QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
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l Similarity 49.9%;
182; Conservative
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Pred. No. 2.08e-111;
76; Mismatches 100;
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A (UYLE-) RIJKSUNIV LEID
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16-JUL-1986; JP-167518.
16-JUL-1986; JP-167518.
(DAIN) Dainippon Pharm K
WPI; 88-068419/10.
P-PSDB; P81342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response, cell growth and activation of protective function Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "not present in
Misc_difference 182..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide 1..18 /label signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R70025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Determined by protein Misc_difference 216..241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tobacco; chitinase; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tobacco chitinase encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1995
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This polypeptide is involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Determined by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
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EP-202425.
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al; fungicide; Cluster-A.
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No. 9.90e-71;
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(UYLE-) RIJKSUNIV LEIDEN.
Apotheker-de Groot M. Bol
Melchers LS. Ponstein AS.
WPI: 95-083454/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was obtd. and for deduced from the Sequence 371.
                                                                                                                                                                                                                                                              29-SEP-1995 (first entry)
Tobacco cluster-A protein encode
Tobacco; chitinase; antifungal;
                                                                                                                                                                                                                                                                                               T 6
R70029 standard;
                                                                                                                                                                                /note- "Determined EP-639642-A.
                                                                                                                                                                                              Misc_difference
                                                                                                                                                                                                             /note= "cDNA encodes additional Misc_difference 188..201
                                                                                                                                                                                                                                                   кеу
                                                                                                                                                          17-AUG-1993;
                                                                                                                                                                                                                            /label= signal peptide
Misc_difference 28..29
                                                                                                                                                                                                                                                           Nicotiana
                                                                                                                                                                                              /label= Determined by sequencing Misc_difference 222..247
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Sela-buurlage M
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27-OCT-1994; U01198.
10-FEB-1994; US-045269.
14-APR-1993; US-045269.
(CORR) CORNELL RES FOUND I
Harman GE, Hayes CK, Lori
                                                                                                                                                                                                                                                            (Eng).

Example 8; Page 45; 62pp; English.

Example 8; Page 45; 62pp; English.

Q78144 encodes R63441 the Trichoderma harzianum pl endochitinase,

which can be used to inhibit chitin containing fungi and chitin

containing herbivorous insects, especially from the genera below

containing Gliocladium, Rhizoctonia, Trichoderma, Uncinula, Ustilage,

Fusarium, Gliocladium, Rapizoctonia, Sclerotium and Alternaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone with the Cluster-A gene revealed that these sequences share a high degree of identity (94%). The Cluster-A precursor protien contains a putative signal peptide as well as 4 potential N-linked glycosylation sites (N.X-S/T). The predicted mature protein has a calculated mol. wt. of 39,033 Da.

Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q78144
Trichoderma harzianum
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06-JUL-1995
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dweyp-addtqatnmvlllkeirsqldayaaqy-apg-yhfllsiaapagpehy-sflhm
||||| :: : | :: :: :| ::|| | || || || : :
                                                                       QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL
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N-linked
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(ERAP ) SOC NAT ELF
Grezes-Besset B, G:
WPI: 94-217870/26.
                                                                                                                                                                                                                                                                                                       The sequence coding for wheat germin, a protein induced during germination of wheat, is a preferred example of DNA coding for protein able to degrade oxalic acid. Such DNA can be coupled to sequence of interest, e.g. one coding for enzymes which confer resistance to pathogens (esp. endochitinases). Plant calli which have been successfully transformed by the sequences are selecte by their ability to grow on oxalic acid-contg. medium. R56861 is a known sequence of a mature endochitinase; the sequence was previously disclosed in EP-531218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxalic acid degradation; oxalate oxidase; filamentous fungus endochitinase; precurso pathogen resistance; plant cell selection
                                                                                                                                                                                                                                                                                                                                                                                                                          cell selection, esp. gene coupled to gene-encodir conferring pathogen resistance Disclosure and Claim 8; Page 39-40; 64pp; French.
                                                                                                                                                                                                                                                                                             previously
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of gene encoding oxalic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q68353.
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07-DEC-1992;
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gcysydpstkelisfdtpamistkvswlkgkglggsmfw
                                           lgmplygrsfq-qt--eg-igkpyngigs-gsw--englwdykalpk-agatvkcddtak
                                                                               QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                           GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                                                                                                                                                       LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
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                           LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELF SAMOFI.
SOC NAT ELF AQUITAINE.
Grison R, Pignard
                                                                                                                                                                                                                                           101;
                                                                                                                                                                                                                                                       Similarity
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FR-014721.
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l. No. 9.31e-42;
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R33068 standard; Prote
R33068;
30-JUN-1993 (first e
                                                                                                                                                                                                                                                                                                                                                                                        mRNA by screening with anti-chitinase antiserum. Three probes were designed based on the CH3C sequence, corresponding to the start, middle and downstream regions of the coding sequence. The probes were used to isolate the full-length coding sequence of A. album endochitinase from an A. album cDNA library in pTZ19R. A 1.6kb fragment was identified in several positive clones. The sequence of the fragment contained an our encoding a 423 amino acid protein. The mature endochitinase can be used to control pathogens such as fungl, bacteria, arthropods and nematodes on plants.
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R33072
R33072
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N-PSDB; Q37711, Q37712.
Recombinant DNA encoding fungal endo:chitinase - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide /note- "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protecting plants against fungi, insects, etc. Claim 1; Fig 1; 75pp; French. Clone CH3C was isolated from a cDNA bank prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SNFI
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06-SEP-1991; FR-011072.
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(ERAP ) SOC NAT ELF AQUITAINE.
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de 23..34
- "pro-sequence"
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22-AUG-1996.
22-AUG-1996; U02332.
13-FEB-1995; US-386727.
4 (UYJO ) UNIV JOHNS HOPKINS.
5 (UYJO B) Chitlaru E, Key
N-PSDB; T36390.

Chitin biosynthetic enzymes end I, exo I and exo II - are periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:gluco:amidase(s), respectively Example 4; Page 79-82; 101pp; English.

Periplasmic chitodextrinase (W02156), periplasmic Beta-N-acetylglucosaminidase (W02157) and aryl

Beta-N-acetylglucosaminidase (W02158) can be used to produce chitin are contactively with the structure (GlcNAc)n where n is 2 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA encoding fungal endo:chitinase - useful for protecting plants against fungi, insects, etc. Claim 22; Page 60-61; 75pp; French.

This mature protein from the filamentous fungus Aphanocladium album has endochitinase activity and is used to control pathogens such as fungi, bacteria, arthropods and nematodes on plants. Recombinant DNA comprising the endochitinase coding sequence is specifically intended for transforming Nicotiana tabacum, Helianthus
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04-SEP-1992; 402414.
06-SEP-1991; FR-011072.
(SNFI ) ELF SANOFI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio furnissii.
W09625424-Al.
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Beta-N-acetylglucosamidase;
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W02159 standard;
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chitin; oligosaccharide; catabolic;
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Best Local
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26-MAR-1984; US-593691.
18-JUL-1986; US-888033.
09-JUL-1990; US-550253.
(DNAP) DNA PLANT TECHNOLOGY CC
Jones JDC, Suslow T.
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                                                                                                                                                                                   Plant cell contg. signal sequence of chitinase A gene - for secretion of foreign polypeptide, esp. chitinase A for protection against pathogenic fungi and nematodes.

Disclosure; Fig. 1A-IC; 20pp; English.
Serratia marcescens QMB1466 genomic DNA was partially digested,
ligated into vector pLAFR1, packaged into lambda phage particles, and used to transfect Escherichia coli DH1 (ATCC 33849) cells.

Plating on chitin medium was used to screen for chitinase activity.

Clone C12 (ATCC 67152) was isolated. Its sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all genes
Sequence
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encoded
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US5374540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitinase A; protein secretion; biological control i transgenic plant; chitin; plant pathogen; nematode; crop protection; pCHIT1251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinase A. Chitinase A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R64823 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q76290
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 95-035648/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serratia marcescens QMB1466
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                                               h 14.3%;
Similarity 28.2%;
91; Conservative
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Similarity 30.7%;
93; Conservative
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                                                                                                                                                                    the deduced protein sequence in
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. No. 3.32e-31;
Mismatches 104;
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                                                  Mismatches
                                                                      389;
No. 2.
                                                                                                                                                                      Its sequence is 
nce in R64823.
                                               DB 12; I
2.18e-24;
ches 126;
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US5290687-A.
01-MAR-1994.
26-MAR-1984; 593691.
26-MAR-1984; US-593691.
18-JUL-1986; US-888033.
09-JUL-1990; US-500253.
14-AUG-1992; US-939970.
(DNAP ) DNA PLANT TECHNOLOGY CO
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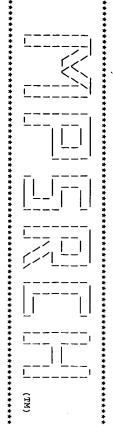
N-PSDB; Q57966.
Inhibition of chitinous fungal plant pathogens - by transforming the chitinase activity plant with DNA encoding chitinase activity plasmid pcHIT1251 containing the chitinase-A gene (chiA), fused directly to a nos promoter, may be used to transform, via Agrobacterium sp., a crop plant. The resulting transgenic plants expressing the chitinase-A protein fragment are protected against fungi, nematodes, insects and disease agents. The protein is fungi, nematodes, insects and disease agents. The protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial chitinase-A fragment from pCHIT1251.
Chitinase-A; enzyme; transgenic plant; biological
disease-resistance; crop improvement; Agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preferably expressed by the plant only at the site of pat attack, e.g. only in the root cells. The plants express chitinase in a biologically active form. Sequence 561 AA;
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N-PSDB; Q57966.
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Pred. 1
84; M
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                                                                                                                                                                                                                                                                                                                                                                                                       372;
No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
.79e-23;
                                                                                                                                                                                                                                                                                                                                                                              125;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
     462
                                                                                                         405
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Best Loc
Matches
                                                                                  22-AUG-1996.
13-FEB-1996; U02332.
13-FEB-1995; US-386727.
(UYJO) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HanPV IE-1 gene protein (partial sequence).
Hellothis armigera nuclear polyhedrosis virus;
insecticide; immediate early-1.
Hellothis armigera nuclear polyhedrosis virus.
W09303144-A.
18-FEB-1993.
18-FEB-1993.
05-AUG-1992; AUO413.
05-AUG-1991; AU-007576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q35982.
Insect virus with reduced capacity to occlude for controlling proliferation of insect pests
                                                                    Yu C;
                                                                                                                                                                                                                                                                    14-JAN-1997 (first entry)
Periplasmic chitodextrinase.
Periplasmic chitodextrinase;
Periplasmic chitodextrinase;
Deta-N-acetylglucosamidase;
WPI; 96-393335/39.
N-PSDB; T36387.
Chitin biosynthetic enzymes
                                                                                                                                                                                                         Vibrio furnissii.
WO9625424-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 51pp;
The sequence is that enconnuclear polyhedrosis viru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSIR ) COMMONWEALTH SCI & IND RES
Christian PD, Dall DJ, Gordon KHJ,
WPI; 93-076501/09.
                                                                                                                                                                                                                                                        catabolism.
                                                                                                                                                                                                                                                                                                                                                                                        T 15
W02156 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (partial sequence).
Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mldq-vqiqtnrtlelttaisagidkiaav-ncdraqqyldkifvmsydfkgawsntdlg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNSPLYKRQEESGAAASLNVDAAVQQWL-QKGTPASKLILGMPTYGRSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVT-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRQTFVNSAI-R-F-L-RKYSFDGLDLDWEYPGSQGS-PAV-DKER----FTTLVQDLAN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              akgkyvldkqlgglfsweidadn 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 10.0%;
Similarity 34.1%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded by the Heliothis armigera (He virus (NPV) immediate early-1 (IE-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                          Keyhani
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                                                                                                                                                                                                                                                                                                                                                                                           1046
  end
                                                                                                                                                                                                                                                                         ; periplasmic Beta-N-acetylglucosaminidase;
chitin; oligosaccharide; catabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 271; DB 6;
Pred. No. 9.19e-14;
43; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343
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    and
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  exo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 238
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Best Local :
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                           periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:gluco:amidase(s), respectively Claim 2; Page 68-71; 101pp; English.
Periplasmic chitodextrinase (W02156), periplasmic
Beta-N-acetylglucosaminidase (W02157) and aryl
Beta-N-acetylglucosaminidase (W02158) can be used to produce chitin oligosaccharides with the structure (GlcNAc)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes endi, exoI and exoII respectively. They are allocated in the catabolic pathway of chitin.
                                                                                                                                                                                                                                                  Sequence
                                                                             454 etfadsavemmrkyrfdgldidlrisnidggtgnpddtafsesrraylmnsyhelmrvlr 513
 204
                                                                147
                                                                                                                                                                                   y Match 8.0%;
Local Similarity 33.3%;
hes 48; Conservative
                                                                                                                         96
                      naalydtgkdselagw-nvygtag
 NSPLYKRQEESGAAASLNVDAAVQ
                                                        QTFVNSAIRFLRKYSFDGLDLD-W--EYPGSQGSPA-VD-KE-RFTTLV---QDLANAFQ
                                                                                                                                                                                                                                                   1046 AA;
                                                                                                                                                                                   Score 219;
Pred. No. 3.
40; Mismatc
 227
                              595
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                   DB 19; I
3.07e-09;
tches 42;
                                                                                                                                                                                                                Length 1046;
                                                                                                                                                                                      Indels
                                                                                                                                                                                     14;
                                                                                                                                                                                   Gaps
                                                                                                                         146
                                                                                                                                                                                      10;
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Search completed: Fri Jun 27 17:04:25 1997 Job time: 74 secs.

•				



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 27 17:01:00 1997; MasPar time 17.84 Seconds 596.027 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-663-618A-14 (1-373) from US08663618A.pep 2721 1 AKLVCYFTNWAQYRQGEARF..........YPLIQTLRQELSLPYLPSGT 373

Scoring table: PAM 150 Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir50

Statistics:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 47.350; Variance 104.053; scale 0.455

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Length	BB	Ħ	Description	Pred. No.
	1488	54.7	383	13	A49562	cartilage glycoprote	8.90e-251
N	1428	52.5	383	16	13	arin-bindi	.76e-23
ω	1417	Ñ	381	14	9	protein -	.51e-23
4	1417	Ñ	381	14	2	protein -	.51e-
տ	1345	ø	399	S	S27879	tory protei	.04e-
σ	1328	48.8	537	14	S57197	pecific q	.60e-
7	1318		539	14	I46470	•	.92e-2
æ	1179		483	12	A53918	chitinase (EC 3.2.1.	1.78e-1
9	1086		504	12	A38221	chitinase (EC 3.2.1.	.90e-
10	1015	37.3	554	12	A56596	ω. 2.	1.05e-160
11	869		699	5	A38368	chitinase (EC 3.2.1.	2.18e-101
12	594	21.8	378	ហ	S51591	chitinase (EC 3.2.1.	2.86e-82
13	582		424	v	S47133	chitinase (EC 3.2.1.	4.43e-80
14	576	21.2	423	u	JQ1975	chitinase (EC 3.2.1.	5.50e-79
15	561		423	12	S51369	chitinase – fungus (ż
16	546	20.1	427	12	JC4565	(EC	6e-7
17	446	16.4	563	16	S60651	chitinase precursor	1.45e-55
18	404	14.8	561	9	A25090	chitinase (EC 3.2.1.	4
19	345	•	799	œ	PC4106	chitinase (EC 3.2.1.	ω
20	344	12.6	499	φ	S52422	chitinase (EC 3.2.1.	w
21	344	12.6	820	16	A40633	(EC 3.2.	1.04e-37

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23
99	99	101	101	101	101	100	104	104	110	112	121	121	136	136	172	172	229	246	263	266	287	314
						3.7			4.0	4.1	4.4	4.4	5.0	5.0	6.3	6.3	8.4	9.0	9.7		10.5	11.5
958	398	1070	1045	662	562	364	422															
Н	σ	11	N	11	ω	11	4	φ	10	16	υ	σ	14	14	3	14	σ	G	11	12	10	11
JN0102	A37768	S19686	SUSEMM	S61193	KRHUEB	S45925	ZWECC	S28440	A41961	S37623	S32039	S33848	S55693	S57204	A37954	A27682	S57715	JC2135	S07915	JC4038	JH0573	S61166
יסי	streptococcal pyroge	alpha-glucosidase (E		probable membrane pr	keratin, 56K type II	hypothetical protein	umuC protein - Esche	probable coproporphy	(EC 3	s wit	w	chitinase (EC 3.2.1.	oviduct-specific sia	oviduct-specific gly	estradiol-stimulated	39K whey protein - b	3.2.	chitinase (EC 3.2.1.	RF2 protein - yeast	47K glycoprotein - f	chitinase (EC 3.2.1.	probable membrane pr
	3.25e+00	1.94e+00	1.94e+00	1.94e+00	1.94e+00	2.52e+00	8.88e-01	8.88e-01	1.77e-01	1.02e-01	7.93e-03	7.93e-03	8.95e-05	8.95e-05	7.80e-10	7.80e-10	1.40e-18	ង	4.45e-24	1.43e-24	4.76e-28	1.37e-32

ALIGNMENTS

lknrnpnlktllsvggwnfgsgrfskiasntgsrrtfiksvppflrthgfdgldlawlyp 142	Db 83 lknrnpnlktl
KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLSTTEWNDETLYQEFNG 61	Qy 2 KLVCYFTNWAC
yregdgscfpdaldrflcthiiysfanisndhidtwewndvtlygmlnt 82	Db 23 klycyytswsc
53.3%; Pred. No. 8.90e-251; vative 83; Mismatches 79;	Best Local Similarity Matches 195; Conser
54.78;	Query Match
#IADEL MAT length 383 #molecular-weight 42613 #checksum 2942	SUMMARY #1er
#product cartilage glycoprotein gp39 #status predicted	22-383
#domain signal sequence #status predicted #label SIG\	1-21
cartilage; extracellular protein; glycoprotein	ω
##residues 22-40,'X',42-45 ##label NY2	##residues
	a
MUID: 90328983	rence
povine mammary protein expressed during the non-lactating period.	99
39 kDa protein	#title Huma
Biochem. J. (1990) 269:265-268	
kos, P.; Golds, E.E.	rs
77	REFERENCE S10677
GB:M80927	##cross-references
1-383 ##label HAK	##residues
mRNA	##molecule_type mRNA
preliminary	Ω
Chitinase protein family.	CARDA COISSEOCH#
3	. c.
Human cartilage gp-39, a major secretory product of articular	
) 268:25803-258	#journal J. I
Hakala, B.E.; White, C.; Recklies, A.D.	S
62	
A49562; S10677; A33162	ACCESSIONS A495
-May-1996 -May-1996	0.3
piens #common_name man	NISM
39K synovial protein	E_NAMES
cartilage glycoprotein gp39 precursor - human	
62 #type complete	ENTRY A49562
	RESULT 1

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ACCESSIONS
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                                                                    GMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRIQDQK
                                                                                 LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
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                                    vpyatkgnqwvgyddqesvknkakylksrqlagamvwtldlddfrgnfcgqnlrfpltsa
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                                                                                                                                                                                                                                                                                                        . Similarity
191; Conser
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submitted to the EMBL Data Library, January 1995
Identification of a 38kba heparin-binding glycoprotein
(gp38k) in differentiating vascular smooth muscle cells
a member of a group of proteins associated with tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $51327 #type complete
heparin-binding glycoprotein 38K - pig
#formal_name Sus scrofa domestica #common_name domestic
07-May-1995 #sequence_revision 07-May-1995 #text_change
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larity 52.2%;
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1-383 ##label
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383 #molecular-weight 42443 #checksum
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Pred. No. 2.76e-239;
81; Mismatches 85;
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#cross-references MUID:95060797
#accession 148271
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Similarity 50.78;
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##CTOSS-Teferences EMBL:X93035
W #length 381 #molecular-weight 43001
                               **scarus preliminary;
##molecule_type mRNA
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                                                                                                                                                                               148271 #type COMPACT.
BRR39 protein - mouse
BRR39 protein - mouse
#formal_name Mus musculus #common_name house
02-Jul-1996 #sequence_revision 02-Jul-1996 #t
02-Jul-1996
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#formal_name Mus musculus #common_name house mouse
10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
03-May-1996
                                                                                                             Morrison, B.W.; Leder, P.
Oncogene (1994) 9:3417-3426
neu and ras initiate murine mammary
markers generally absent in c-myc
                         1-381 ##label
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protein - mouse
           EMBL: X93035;
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Pred. No. 3.51e-237;
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RES; NID:g1085065;
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[FICATION #superfamily Streptomyces chitinase chi40
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##residues 1-399 ##label CHA
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Similarity 47.78;
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Similarity 50.7%;
186; Conservative
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secretcy protein YM-1 precursor - mouse
secretcy musculus #common_name house
#formal_name Mus musculus #common_name house
17-Apr-1993 #sequence_revision 17-Apr-1993 #t
03-May-1996
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#length 381 #molecular-weight 43001
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Pred. No. 3.51e-237;
84; Mismatches 86;
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Pred. No. 2.04e-223;
87; Mismatches 102;
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Query Match

Best Local Similarity 51.2%;
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## #length 537 #checksum 1695
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##residues 1-537 ##label
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S57197
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#formal_name Bos primigenius taurus #common_name cattle
28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
03-May-1996
$57197
$57197
$endai, Y.; Abe, H.; Kikuchi, M.; Satoh, T.; Hoshi, H.
Biol. Reprod. (1994) 50:927-934
Purification and molecular cloning of bovine oviduct-spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S57197 #type oviduct-specific
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Pred. No. 3.60e-220;
74; Mismatches 97;
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glycoprotein
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#journal
#title
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#cross-references MUID:95269691
                            #accession
                                                         #title
                                                                                    #authors
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##residues 1-539 ##label DES
##molecule_type
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                ##status
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##cross-references EMBL:U16719; NID:g885600; CDS_PID:g885601
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1 Similarity 50.18;
183; Conserver
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estrogen dependent oviduct protein precursor - sheep
#formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
                            stored
A53918
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chitinase
                                                                                                                          #formal_name Chelonus sp.
28-Jul-1995 #sequence_revision
03-May-1996
                                       Krishnan, A., Nair, P.N.; Jones, D.
J. Biol. Chem. (1994) 269:20971-20976
Isolation, cloning, and characterization of new chitinase
stored in active form in chitin-lined venom reservoir.
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Endocrinology (1995) 136:2485-2496
An estrogen-dependent secretory pr
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(EC 3.2.1.14) precursor -
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Pred. No. 2.92e-218;
77; Mismatches 98;
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##note sequence extracted from NCBI backbone
iDS glycosidase; hydrolase
ty #length 504 #molecular-weight 55971 #che
                                                                                                                                                                                                           ##status preliminary; not compared
##molecule_type nucleic acid; protein
##residues 1-504 ##label FUH
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                                                                aemsqyldfinlmtydfhgpwdghtgmhappsasshdsgnelklnvkaavkywlqngvpk
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eklvvgvpaygksftlsnpsnkglgapvsgagtagpytgengllgyneicemqkagdwev
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                                                                                                  39.9%;
l Similarity 42.8%;
158; Conservation
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Similarity 42.5%;
158; Conservative
                                                                                                                                                                                                                                                                         Fuhrman, J.A.; Lane, W.S.; Smith, Perler, F.B. Proc. Natl. Acad. Sci. U.S.A. (19 Transmission-blocking antibodies chitmase in brugian lymphatic
                                                                                                                                                                                                                                                                                                                                                                                    A38221 #type complete
Chitinase EG 3.2.1.14) MF1 - r
#formal_name Brugia malayi
04-Mar-1993 #sequence_revision
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#length 483 #molecular-weight 52013
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                                                                                                     Score 1086;
Pred. No. 3.
94; Mismatc
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Pred. No. 8.78e-192;
98; Mismatches 99;
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                                                                                                      Mismatches 102;
                                                                                                                  3.90e-174;
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                                                                                                                               DB 12;
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Similarity 40.4%;
155; Conservative
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Insect Blochem. Mol. Biol. (1993) 23:691-701
Sequence of a cDNA and expression of the gene encoding
epidermal and gut chitinases of Manduca sexta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence extracted from NCBI backbone glycosidase; hydrolase #length 554 #molecular-weight 62203 #checksum 4659
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chitinase (EC 3.2.1.14) - tobacco hornworm
formal_name Manduca sexta #common_name tobacco hornworn
11_Aug-1995 #sequence_revision 11-Aug-1995 #text_change
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Pred. No. 1.05e-160;
98; Mismatches 107;
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                ##molecule_type mRNA
##residues 1-378 ##label_HEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 qlnkikqtnpnlktiisvggwtw-snrfsdvaataatrevfansavdflrkynfdgvdld 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-699 ##label WAT
##cross-references GB:J05599
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##cross-references EMBL:X78325
                                                                                                                                                                                                                                                                                                                                                                                                                          288 W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 GYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPL-YKRQE-ESGAA-A-SLNVDAAVQQ 228
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l Similarity 40.1%;
l19; Conservative
                                                                                                                                                                                                                                                    ships a type complete chitinase (EC 3.2.1.17) PZ precursor pathogenesis-related - common tobacco formal_name Nicotiana tabacum #common_name common tobacco formal_name revision 08-Sep-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. (1990) 265:15659-15665
Gene cloning of chitinase Al from Bacillus circulans
revealed its evolutionary relationship to Serratia
chitinase and to the type III homology units of
                                                                         V.; Brunner, F.; Fritig, B.; Legrand, M.
Mol. Gen. Genet. (1994) 245:246-254
Molecular characterization of a novel tobacco
pathogenests-related (PR) protein: a new placehitinase/lysozyme.
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S51591
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chitinase (EC 3.2.1.14) precursor - Bacillus
#formal_name Bacillus circulans
28-Jun-1991 #sequence_revision 28-Jun-1991 #t
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##residues 31-36;87-112;252-275;282-305;337-371 ##label
CLASSIFICATION #superfamily Streptomyces chitinase chi40
KEYWORDS glycosidase; hydrolase
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cession S51632
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qlfk-lkkanrnlkvmlsiggwtwst-nfpsaastdanrknfaktaitfmkdwgfdgidv 169
| |: || | : || :|: :| || :| :| || :: :|| |::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQR-IQDQK-VP-YIFRDNQWVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a-dttaygimarqpnsrksfidssirlarqfgfhgldldweyp--1-s-atdmtnlgill 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nnidstlfthlfcafadlnpqsnqliispenqds-fsqftstvqrknpsvktflsiaggr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLDPSLCTHLIYAFAGMT--NHQLSTTEWNDETLYQEFNG-LKKMNPKLKTLLAI-GGW 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYPGSQGSPAVDKERFTTLV
                                              102;
                                           h 21.4%;
Similarity 36.0%;
102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 21.8%;
Similarity 32.7%;
106; Conservative
                                                                                                                                                                                                                                                            $47133
$47133
Carsolio, C.; Gutierrez, A.; Jimenez, B.; van Montag
Herrera-Estrella, A.
submitted to the EMBL Data Library, June 1994
Characterization of ech-42, a Trichoderma harzianum
                                                                                               48/2; 81/2; 98/1
#superfamily Streptomyces chitinase chi40
glycosidase; hydrolase
#length 424 #molecular-weight 46298 #checksum
                                                                                                                                                                                                                                 endochitinase gene
S47133
                                                                                                                                                                                                                                                                                                                                                          S47133 #type complete chitinase (EC 3.2.1.14) - fungus (Trichoderma #formal_name Trichoderma harzianum 23-Nov-1994 #sequence_revision 03-Aug-1995 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #length
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experimental #label pRO
)th 378 #molecular-weight 42019 #checksum
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                                                                                                                                                                          1-424 ##label CAR
es EMBL:X79381
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Pred. No. 2.86e-82
87; Mismatches 10
                                           Pred.
                                                          Score 582; DB 5;
Pred. No. 4.43e-80;
                                            Mismatches
                                                                                                                                                                                                                                               expressed
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#label
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1-34
35-423
SUMMARY
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GENETICS
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FEATURE
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REFERENCE
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Best Local Similarity 36.2%;
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession JQ1975
##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
 301
                                 340
                                                                241
                                                                                               288
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                                                                                                                                                                                                                                                                           115 lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-423 ##label
##cross-references GB:X64104
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                                                                                                                                                                                                              -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-1g 228
                                                                                                                                                                                                                                                        LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       svaqayysydpsskelisfdtpdmintkvsylknlglggsmfw 379
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                                                                                 lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak 339
                                                                                                                                            kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv 287
                                                                                                                                                                                          GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVW 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
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 VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                               gcysydpstkelisfdtpamistkvswlkgkglggsmfw
                                                              LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                        101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chi1
47/2; 80/2; 97/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaiseau, P.L.; Lafay, J.F.
Gene (1992) 120:243-248
Primary structure of a chitinase-encoding gene (chil) from
the filamentous fungus Aphanocladium album: Similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JQ197
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                                                                                                                                                                                                                                                                                                                                                                                    #domain signal sequence #status predicted #label
#product chitinase 1 #status predicted #label MN
#length 423 #molecular-weight 40072 #checksum 8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily Streptomyces
glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                       Score 576; DB 5; Length 423; Pred. No. 5.50e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degradation of insoluble chitin.
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                                                                                                                                                                                                                                                                                                                        95;
 337
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ACCESSIONS
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Search completed: Fri Jun 27 17:02:53 1997 Job time: 113 secs.
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ENTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #accession S51305
##status preliminary
##molecule_type DNA
##residues 1-423 ##label GAR
##residues #length 423 #molecular-weight 46056 #checksum 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.6%; Score 561; DB 12; Length 423; Best Local Similarity 35.7%; Pred. No. 2.95e-76; Matches 101; Conservative 71; Mismatches 94; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal
#title
                                                                        336 svakgyysynsatkelisfdtpdmintkvaylkslglggsmfw 378 | | : ::|| : ::|||:|| | ||||:| | 297 QDQKVPYIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW 337
                                                                                                                                                169 dweyp-adatqasnmillikevrsqrdayaaqy-apg-yhfiltiaapagkdny-skiri 224
||||| :::: | :: |: ::| ::|| :|| |||
117 DWEYPGSQGSPAYDKERETTLYQDLANAFQQEAQTSGKERLLLSAAVPAGQTYYDAGYEV 176
                                                                                                                                                                                                                                                                                                                                                                                               111 qlfk-vkkanrglkvllsiggwtwst-nfpsaastdanrknfaktaitfmkdwgfdgidi 168
                                                                                                                                                                                                                                                                                                                                                                            57 QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garcia, I.; Lora, J.M.; de la Cruz, J.; Benitez, T.; Llobe A.; Pintor-Toro, J.A. Curr. Genet. (1994) 27:83-89 Cloning and characterization of a chitinase (CHIT42) cDNA from the mycoparasitic fungus Trichoderma harzianum. S51369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $51369  #type complete
Chitinae fungus (Trichoderma harzianum)
#formal_name Trichoderma harzianum
15-Jul-1995  #sequence_revision 19-Apr-1996  #text_change
03-May-1996
$51369
$51369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.; Benitez, T.; Llobell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps 13;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 27 16:59:40 1997; MasPar time 12.05 Seconds 656.435 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence:

>US-08-663-618A-14
(1-373) from US08663618A.pep
2721
1 AKLVCYFTNWAQYRQGEARF......YPLIQTLRQELSLPYLPSGT 373

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries 59021 seqs, 21210388 residues

Searched:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.978; Variance 85.387; scale 0.574

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 110 110 110 110 110 110	Result No.
1488 1015 698 551 546 433 337 337 263 172 172 172 172 172 172 172 172 172 172	Score
354 354 37 337 337 337 337 337 337 337 337 337	Query Match
383 554 699 423 423 551 551 1146 610 1146 610 1146 620 427 427 427 427 427 427 427	Length
110 110 1110	B
GP39_HUMAN CHIT_BRUMA CHIT_MANSE CHIL_BACCI CHIL_BACCI CHIL_TRIHA CHIT_COCIM CHIR_SERMA CHIT_NPVAC CHIB_SERMA CHIT_STRPLI CHIT	ID
CARTILAGE GLYCOPROTEI ENDOCHITINASE PRECURS CHITINASE A1 PRECURSO CHITINASE A1 PRECURSO CHITINASE A1 PRECURSO CHITINASE A1 PRECURSO 42 KD ENDOCHITINASE D ENDOCHITINASE A PRECURSOR CHITINASE B PRECURSOR CHITINASE B PRECURSOR CHITINASE G3 PRECURSOR CHITINASE G1YCOPROTEI ESTRADIOL-DEPENDENT O EXOCHITINASE 1 PRECUR COPROPORPHYRINOGEN II CHITINASE D PRECURSOR UMUC PROTEIN. HYPOTHETICAL 40.9 KD EXTRACELLULAR SERINE	Description
0.00e+00 6.23e-202 4.86e-202 1.82e-127 2.58e-99 6.68e-96 6.175e-92 6.175e-92 6.176e-48 8.67e-48 8.67e-48 8.67e-48 8.67e-43 8.27e-13 8.27e-13 8.27e-13 8.27e-13 8.27e-13 9.29e-01 1.13e-02	Pred. No.

Ş 밁

Matches

195;

Conservative

83; Mismatches

79;

Indels

9;

Gaps

5

4.4 5	43	42	41	40	39	38	37	36	35	34	ယ္သ	32	31	30	29	28	27	26	25	24	23
92	9 9	93	95	94	95	95	95	96	95	94	95	94	96	98	99	97	97	97	98	99	101
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ERK3_HUMAN	YHO8_YEAST	EBAG_FLASP	VGR1_MOUSE	YAJ1_SCHPO	K2CF_HUMAN	K2CE_HUMAN	HYES_MOUSE	HYES_RAT	PDI_SCHPO	MOEA_HAEIN	YQHT_BACSU	GCH2_PICGU	HMX1_HUMAN	PRTS_SERMA	AMYG_SCHOC	K2CC_HUMAN	K2CA_HUMAN	K2CB_HUMAN	SYK_THETH	SPEB_STRPY	AGLU_CANTS
EXTRACELLULAR SIGNAL-	HYPOTHETICAL 35.1 KD	ENDO-BETA-N-ACETYLGLU	VASCULAR ENDOTHELIAL	PUTATIVE FAMILY 31 GL	KERATIN, TYPE II CYTO	KERATIN, TYPE II CYTO	SOLUBLE EPOXIDE HYDRO	SOLUBLE EPOXIDE HYDRO	PUTATIVE PROTEIN DISU	MOLYBDOPTERIN BIOSYNT	PUTATIVE PEPTIDASE IN	GTP CYCLOHYDROLASE II	HOMEOBOX PROTEIN MSX-	EXTRACELLULAR SERINE	GLUCOAMYLASE 1 PRECUR	, TYPE II	KERATIN, TYPE II CYTO	KERATIN, TYPE II CYTO	LYSYL-TRNA SYNTHETASE	EXOTOXIN TYPE B PRECU	ALPHA-GLUCOSIDASE PRE
4.41e+00 4.41e+00		3.30e+00	1.83e+00	2.46e+00	1.83e+00		1.83e+00	1.36e+00	1.83e+00	2.46e+00	1.83e+00	2.46e+00	1.36e+00	7.40e-01	5.44e-01	1.00e+00	1.00e+00		7.40e-01	5.44e-01	2.92e-01

ALIGNMENTS

Be D	SQ	H	X E	R	DR	밁	38	ဥ	င္ပ	6	38	S	ဂ္ဂ	RL	RA A	RX	RP	R	R.	RA A	RX.	R	RP :	R C	38	20	DE	D !	ָלְ נָּ	A	ID	RESULT
Query Match Best Local Similarity	CARBOHYD SEQUENCE	CHAIN	GLYCOPROTEIN; SIGNAL.	PROSITE; PS01095; CHITINASE_18	PIR; A33162;	PIR; S10677	-!- SIMILAR	7	-!- PTM: GI	PANCREA	-!- TISSUE	RESPOND	-!- FUNCTIO	віоснем. J. 269:265-268(1990).	NYIRKOS P.,	MEDLINE; 90328983.	SEQUENCE OF	[2]	J. BIOL. CHEM. 268:25803-25810(1993).	HAKALA B.E.	MEDLINE; 94064658.		UENCE	[1]	EUNAKYOTA; METAZOA; CHORDATA; VERTEBRATA;	HOMO SAPIENS (HUMAN).	CARTILAGE GLYCOPROTEIN-39	01-OCT-1996	01-JUN-1994	P36222; P30923;	GP39_HUMAN	LT 1
	60 383 AA;		N; SIGNAL	01095; СН	; A33162.	S10677; S10677.	TY: BELC	ULAR LOCA	PTM: GLYCOSYLATED.	S, MONONU	SPECIFICI	TO AND C	N: MAY PI	269:265-	GOLDS E.	328983.	22-45.		EM. 268:2	, WHITE C	064658.		FROM N.A.,		METAZOA;	S (HUMAN)	LYCOPROTE		(REL. 20	923;	STANDARD;	
54.78; 5	60 42613 MW;	383	<u>.</u> :	ITINASE_1			NGS TO FA	TION: EXT	ð	CLEAR CEI	TY: PRESE	OPE WITH	AY AN IMI	268(1990)	H .				5803-2581	., RECKL			AND PARTIAL		CHORDATA;		N-39	LAST AN	LASTEL		ARD;	
Score 1488; Pred. No. 0	POTENTIAL. DOA5280F	CARTILAGE		.8			SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES	SUBCELLULAR LOCATION: EXTRACELLULAR.		PANCREAS, MONONUCLEAR CELLS, OR FIBROBLASTS	TISSUE SPECIFICITY: PRESENT IN ARTICULAR CHONDROCYTES, SYNOVIAL	RESPOND TO AND COPE WITH CHANGES IN THEIR ENVIRONMENT.	FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE CAPACITY OF	•					0(1993).	ES A.D.;			AL SEQUENCE		VERTEBRA		PRECURSOR (GP-39) (39	NOTATION	(REIL 29 LART SECHENCE HUDDATE)		PRT; 3	
1488; DB 4; No. 0.00e+00;		GLYCOPROTEIN-39					F GLYCOS	IR.		BROBLASTS	TABLE TO	N THEIR E)LE IN THE										Œ.		TA; TETRA		P-39) (39	UPDATE)	DATE:		383 AA.	
Length		TEIN-39.					L HYDROL		,	S. MOOCHU A.	MISCLE	ENVIRONMEN	CAPACITY												TETRAPODA; MAMMALIA;		KD SYNOVIAL					
383;							ASES.			, בי	SS, SYNOVIAL	AT.	OF CELLS												MALIA;		/IAL PROTEIN)					
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Best Local S
Matches 15
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O1-DEC-1992 (REL. 2
O1-DEC-1992 (REL. 2
O1-FEB-1995 (REL. 3
O1-FEB-1995 (REL. 3
                                                                                   DOMAIN
ACT_SITE
SEQUENCE
                                                                                                                               CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE; 92179220.

FUHRMAN J.A., LANE W.S., SMITH R.F., PIESSENS W.F., PERLER F
PROC. NATL. ACAD. SCI. U.S.A. 89:1548-1552(1992).

-1- FUNCTION: THE MF1 ANTIGEN IS A MICROFILARIAL CHITINASE,
FUNCTION TO DEGRADE CHITIN-CONTAINING STRUCTURES IN THE
FILARIA OR IN ITS MOSQUITO VECTOR DURING PARASITE DEVELO
                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA;
                                                                                                                   DOMAIN
                                                                                                                                                     SIGNAL
                                                                                                                                                                                                         EMBL;
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 5
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DEVELOPMENTAL STAGE: THE APPEARANCE OF THE MF1 ANTIGEN CORRESPOND WITH THE ONSET OF THE PARASITE'S ABILITY TO INFECT THE MOSQUITO. SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                           TRANSMISSION.
CATALYTIC ACTIVITY:
                                                                                                                                                                                            L; M73689;
A38221; A
                                                                                                                                                                                                                                                                     N-ACETYL-D-GLUCOSAMINE POLYMERS PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                                   HYDROLASES)
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                                         h 39.9%;
Similarity 42.8%;
158; Conservative
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PS01095; C
                                                                                                                                                             GLYCOSIDASE; CHITIN DEGRADA
YCOPROTEIN; CALCIUM-BINDING
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.ECURSOR (EC 3.2.1.14)
                                                                                                                                                                       CHITINASE_18. IDASE; CHITIN
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                                         Score
Pred.
94; M
                                                                                            CATALYTIC.
SER/THR-RICH (LINKER).
3 X 14 AA APPROXIMATE TANDEM
PROTON DONOR (BY SIMILARITY).
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                                        e 1086; DB 2; I
1. No. 6.23e-219;
Mismatches 102;
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  Query Ma
Best Loc
Matches
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01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-JUN-1995 (REL. 21, LAST ANNOTATION UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; LEPIDOPTERA
                                              HYDROLASE;
SIGNAL
CHAIN
DOMAIN
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93357793.

KRAMER K.J., CORPUZ L., CHOI INSECT BIOCHEM. MOL. BIOL. 2
-!- FUNCTION: DIGEST CHITIN
                                                                                                                                                              HSSP; P07254; 1CT: PROSITE; PS01095;
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             Local
                                                                                                                                                                                                                    BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A RAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LOW LEVELS SEEN ON DAYS 0, 7 AND 8.

TISSUE SPECIFICITY: EPIDERMIS AND GUT.
SUBCELLULAR LOCATION: SECRETED.
SUBCLILIAR LOCATION: SECRETED.
SUBCLILIAR ICCATION: SCRETED.
                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS
                                                                                                                                                                                                             HYDROLASES)
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   l Similarity
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303
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545
 37.3%;
larity 40.4%;
Conservative
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                                                                                                                                                  CHITINASE_18.
IDASE; CHITIN DEGRADATION;
                                                62203
                                                                                                                                                                                                                                                                                                                                               CHOI H.K., MUTHUKRISHNAN OL. 23:691-701(1993).
                                               WW.
Score 1015;
Pred. No. 4.8
98; Mismatcl
                                             SER/THR-RICH.
PROTON DONOR
PROTON IAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
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  Mismatches
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 DB 2; I
1.86e-202;
ches 107;
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Mon

Jun

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Gaps

18;

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RESOLATION OF THE PROPERTY OF 
Query Match
Best Local
                                                                                                       ACT_SITE
MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
Similarity
25.7%;
40.1%;
                                                                                                              73677
                                                                                                              ₹
Score
Pred.
                                 698;
   ŏ.
DB 2; L'
..82e-127;
                                                                                                          CRC32;
                                 Length
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EMBL;

M57601;

PS01095;

MUTAGENESIS.

18

OF GLYCOSYL

18;

Gaps

16;

121

287 180 228 ¥.;

õ

WATANABE

BIOL.

SEQUENCE FROM N.A. PROKARYOTA;

CHAIN

DOMAIN SIGNAL HYDROLASE;

```
MEDLINE; 9366760.

WATANABE T., KOHORI K., MIYASHITA K., FUJII T., SANALA, UCHIDA M., TANAKA H.;

J. BIOL. CHEM. 268:18567-18572(1993).

-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN:
                                                                                                                                                                                                                                                                                                                  PIR; A38368; A38368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHITINASE A1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS CIRCULANS
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T., SUZUKI K., OYANAGI W.,
CHEM. 265:15659-15665(1990)
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I ANNOTATION (
C 3.2.1.14).
                                                                           CHITINASE A1.

CATALYTIC.

FIBRONECTIN TYPE-III (R-1).

FIBRONECTIN TYPE-III (R-2).

PROTON DONOR (PROBABLE).

D-N: DECREASE IN ACTIVITY.

D-SE: NO CHANGE IN ACTIVITY.

E-D-D; CLOSS OF ACTIVITY.
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P32470;
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01-FEB-1996
CHITINASE 1
                                                                                                                                                                                                                                                                         CHAIN
ACT_SITE
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BLAISEAU P.-L., LAFAY
GENE 120:243-248(1992)
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BLAISEAU P.-L., KUNZ C., GRISON CURR. GENET. 21:61-66(1992).
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MEDLINE; 930130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 35-57.
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llarity 36.2%;
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(EC 3.2.1.14).
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POTENTIAL.
CHITINASE 1.
PROTON DONOR
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No. 2.50e-99
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SIGNAL 1
PROPEP 23
CHAIN 35
ACT_SITE 171
CARBOHYD 218
SEQUENCE 423 AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHIT42.
TRICHODERMA HARZIANUM.
TRICHOMPERMA: FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PINTOR-TORO J.A.;
CURR. GENET. 27:83-89(1994).
-!- FUNCTION: MORPHOGENETIC ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE MEDLINE; 95269313.
GARCIA I., LORA J.M., LA CRUZ J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S78423; G999376; - HYDROLASE; GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                           336
                                                                                      237
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                                                                                                                                                                                                                                                                                                                                                                                 340
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    297
                                                                                                                                 284
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                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                               169
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                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-ACETYL-D-GLUCOSAMINE I
SUBCELLULAR LOCATION: SI
INDUCTION: SPECIFICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO CHITINASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: MORPHOGENETIC ROLE DURING APICAL GROWTH, CELL DIVISION AND DIFFERENTIATION (CELL WALL MORPHOGENESIS). ANTIFUNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENT.
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                                                                                                             QDQKVPYIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                             DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
                                                                                                                                                                                                                                                                 QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcysydpstkelisfdtpamistkvswlkgkglggtmfw 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak
                                                                                      SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPYIF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            20.6%;
larity 35.7%;
Conservative
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34
423
171
218
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PROTON DONOR (BY S
POTENTIAL.
POTENTIAL.
W; 899DA50A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 561; DB 2;
Pred. No. 6.68e-96;
71; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KD ENDOCHITINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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SGREDITAC

CHIA_SERMA P07254; 01-APR-1988 01-FEB-1995 01-FEB-1995 CHITINASE A

(REL. 07, (REL. 31, (REL. 31, PRECURSOR

07, CREATED)
31, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
RSOR (EC 3.2.1.14).

STANDARD;

PRT;

563 AA

SERRATIA MARCESCENS

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RESULT
ID CHILCCOIM STANDARD; PRT; 427 AA.
AC C94196;
DT 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE COCCIDIOLES IMMITIS
CC COCCIDIOLES IMMITIS
CC COCCIDIOLES IMMITIS
CC CUKARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).

RN (1)
RN (2)
RN MEDLINE; 96144270.
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RN (2)
RN MEDLINE; 96144270.
RN (2)
RN MEDLINE; 96144270.
RN (2)
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Best Local
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||| ||||||| || :|| :| : : :::: | || : : | || :|:
QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                            VPYIF-RDNQW-VGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                        asysydknkrylisydtvkiagkkaeyitkngmgggm-w
:| : :::: :::| | | |: :|:||:| |
                                                                                                                                                                               ede-kgandfvlllkacrealdaysak-hpngk-kflltiaspagpqny-nk-lklaemd
8
                                                                                                                                                                                                                                                                                                                                                                                                       GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%;
Similarity 34.1%;
95; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
ENDOCHITINASE 1.
POTENTIAL
POTENTIAL
SMCSLECLECELGREMETLSTVTAVTVVTDDIQ -:
SMCSMPNYPVPEAPEGGERSVVYFVNW (IN RE)
K -> N (IN REF. 2).
MW; 6CB9AF73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
71; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 546; DB 2;
Pred. No. 1.75e-92;
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                                                                            337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427;
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Query Match
Best Local S
Matches 9
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CONFLICT
CONFLICT
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ACT_SITE
CONFLICT
CONFLICT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE 2:1169-1180(1994).

- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES
- N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE; 95219379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
JONES J.D.G., GRADY K.L.,
EMBO J. 5:467-473(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. KOO J.C., LIM C.O., CHO M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROKARYOTA; GRACILICUTES; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JAN-1993) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VORGIAS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERRAKIS A., TEWS I., DAUTER Z.,
 321
                    523
                                        266
                                                            464
                                                                               206
                                                                                                  406
                                                                                                                      148
                                                                                                                                          349
                                                                                                                                                                                  290
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P; P07254; 1CTM
                                                                                                                    lsaetgr-kyeltsaisagkdkidkvaynvaq--nsmdhiflmsydfygpfdlknlghqt
: :|::|::|::| :| :|:| :| :|:|
EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KYTGHNS
                                                                                                                                                                    akgkyvldkqlgglfsweidadn
                                                                                       alnapawkpdtayt-tvng-vnallaggvkpgkvvvgtamygrgwtgvngygnnipftgt
                                                                                                                                                             NRQTFVNSAIRFLRKYSF-DGLDLDWEYPGSQGS-PAV----DKERFTTLVQDLANAFQQ
                                                                                                                                                                                                    AFAGMTNHQLSTTEWNDE-T-LYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATAN
TKVSYLKQKGLGGAMVWALDLDD
                                       GSGTPGPFTKEGGMLAYYEVCS-WKGATKQ-RIQD-QKVPYIFR-DN-QWVGFDDVESFK
                                                                              PLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPAT
                                                                                                                                                                                                                                                       Similarity
                                                    GLYCOSIDASE;
                                                                                                                                                                                                                                            16.1%;
larity 28.8%;
Conservative
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                                                                                                                                                                                                                                                                                                        437
467
473
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563
315
391
391
139
226
430
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                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                               V -> I (IN REF. 2).
P -> A (IN REF. 1 AND 2).
PAWKPDTAYTTYNGVNALLAQ -> RE
AAGQ (IN REF.1 AND 2).
V -> I (IN REF. 2).
ATGP -> HRA (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                        CHITINASE A.
CATALYTIC.
PROTON DONOR (PROBABLE).
PROBABLE.
TA -> GP (IN REF. 2).
A -> P (IN REF. 2).
V -> I (IN REF. 2).
V -> A (IN REF. 1 AND 2).
                                                                                                                                                                                                                                          Score 437; DB 2;
Pred. No. 6.12e-68;
84; Mismatches 123
                                                                                                                                                                                                                                                                                            ATGP -> HRA
K -> E (IN
G -> S (IN
                    545
343
                                                                                                                                                                                                                                                                                     7764DB57
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                                                                                                                                                                                                                                            Mismatches 123;
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                                                                                                                                                                                                                                                                                             REF. 2).
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                                                                                                                                                                                                                                                                                     CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BANKS
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RESULT 9

ID CHIT_NPVAC
AC P41684;
DT 01-NOV-1995
DT 01-NOV-1995
DE PROBABLE EN
OS AUTOGRAPHA (
OC VIRIDAE; DS
RN [1]
RP SEQUENCE FR
RC STRAIN-C6;
RX MEDLINE; 94
RA AYRES M.D.,
RL VIROLOGY 20)
CC -1- CATALYT
CC -1- CATALYT
CC -1- CATALYT
CC -1- SITILAR
DR EMBL; L2285;
DR PROSITE; PSS
KW HYDROLASE; OS
KW HYDROLA
RESULT
AC COLOR
DT 000

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                                                                                                                     CHIA_ALTSO
P32823;
O1-OCT-1993
O1-OCT-1993
O1-FEB-1995
CHITINASE A
CHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P41684;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS
VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYRES M.D., HOWARD S.C., KUZIO J., VIROLOGY 202:886-605(1994).
-i- CATALYTIC ACTIVITY: HYDROLYSIS N-ACETYL-D-GLUCOSAMINE POLYMER:
-i- SIMILARITY: BELONGS TO CHITINA.
   VIBRONACEAE [1]
                                                            ALTEROMONAS PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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ANNRQTEVNSAIRELRKYSF-DGLDLDWEYPGSQGS-PAV-D-K-E-R-FTTLVQDLANA
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TE; PS00014; ER_T
TE; PS01095; CHIT
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95; Conse
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                                                                                                                                                  (REL. 27, CREATED)
(REL. 27, LAST SEQUENCE UI
(REL. 31, LAST ANNOTATION
PRECURSOR (EC 3.2.1.14) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 AA;
                                                            SP. (STRAIN OGRACILICUTES;
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larity 29.2%;
Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
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CHITINASE_18.
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                                                            SCOTOBACTERIA;
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Pred.
80; M
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No. 1.16e-58;
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S OF CHITIN.
SE CLASS II (FAMI
                                                                                                                                                  ON UPDATE)
(CHI-A).
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EUBACULOVIRINAE.
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                                                         ANAEROBIC
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Best Local (
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                                                                                                                                                                                                                                                         LT 11
CHIB_SERMA
P11797;
01-OCT-1989
01-OCT-1989
01-FEB-1995
CHITINASE B
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                                CHAIN
ACT_SITE
SEQUENCE
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PIR;
                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
MEDLINE; 89345110.
                                                                                                                                                                                               ENTEROBACTERIACEAE
                                                                                                                                                                                                             SERRATIA MARCESCENS.
PROKARYOTA; GRACILICUTES;
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TSUJIBO H., ORIKOSHI
                EMBL;
                                                                                                                                                                                                                                               CHIB.
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                              HYDROLASES)
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ENZYME REGULATION: STIMULATED BY MG2+;
N-BROMOSUCCINIMIDE AND 2-HYDROXY-5-NITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS
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S04856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLY
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P07254; ICTN.
                x15208;
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93106952.
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GLYCOSIDASE; CHITIN
                                                                                                                                                                                                                                                           (REL. 12,
(REL. 12,
(REL. 31,
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KAMI Y., INAMORI Y.;
L. 175:176-181(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YOSHIDA Y., MIYAMOTO K., 
ROBIOL. 38:891-897(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                G47228;
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313
87346
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LAST SEQUENCE UP
LAST ANNOTATION
R (EC 3.2.1.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO CHITINASE CLASS II (FAMILY 18
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INE POLYMERS OF CHITIN.
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                                                                                                                                                                                                             SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 345;
Pred. No. 8.
44; Mismatc
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RATURE OF CHI-A ARE
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838F6EE8 CRC32;
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Best Loc
Matches
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Best Local
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01-JUN-1994
01-JUN-1994
01-FEB-1995
CHITINASE C
                                                                                                              SIGNAL
CHAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
SEQUENCE
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SEQUENCE
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HYDROLASE; GLYCOSIDASE; CHITIN DEGRADATION;
SIGNAL
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41
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                                                                                                                                                                                              EMBL; D12647; G391910;
HSSP; P07254; 1CTN.
PROSITE; PS00018; EF_H;
PROSITE; PS00561; CBD_I
                                                                                                                                                                                                                                                                                                                                                          PROKARYOTA;
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- CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                       HYDROLASES).
SIMILARITY:
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          WNDETLYQEFNGLKKMN----PKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFL
RKYS-FDGLDLDWEYPGSQG-S--PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAA
                                                                        h 11.18;
Similarity 28.28;
86; Conservative
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                                                                                                                                                                       PS00018; EE_HAND.
PS00561; CBD_BACTERIAL.
PS01095; CHITINASE_18.
PS01095; CHITIN DEGRADATION;
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(REL. 29,
(REL. 31,
PRECURSOR
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144
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llarity 34.0%;
Conservative
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IIVITY: HYDROLYSIS OF TH
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144 P
55464 MW;
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, LAST SEQUENCE UPI
, LAST ANNOTATION (
R (EC 3.2.1.14).
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                                                                                                                         CELLULOSE-BINDING.
FIBRONECTIN TYPE-III.
CATALYTIC.
PARAFFIC.
                                                                                                                                                                                                                                            FIBRONECTIN TYPE
                                                                                                                                                                                                                                                                       CHITINASE CLASS
                                                                        Score 301; DB 2;
Pred. No. 2.01e-38;
65; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 337; DB 2;
Pred. No. 4.53e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTON DON
                                                                                                                                                          POTENTIAL.
CHITINASE
                                                                                                             PROTON DONOR (BY 23E3E1EC CRC32;
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                                                                                                                                                                                                                                             TYPE III-LIKE
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                                                                                                                                                                                                                                                      III-LIKE
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R HSSP; D40573; .....

R HSSP; P67254; lCTN.

R HSSP; P67254; lCTN.

R PROSITE; P500018; EF_HAND.

DR PROSITE; P5001055; CHITINASE_18.

DR PROSITE; P5001055; CHITINASE_18.

ET CHAIN 31 610 CHITINASE 63.

FT CHAIN 35 140 CELLULOST-BINDING; SIGNAIN 148 229 FIBRONECTIN TYPE-III.

DOMAIN 236 610 CATALTIC.

TO DOMAIN 236 33 383 PROTON DONOR (BY SIMILARITY).

POMAIN 35 140 CF1BRONECTIN TYPE-III.

TO DOMAIN 236 F1BRONECTIN TYPE-III.

TO DOMAIN 35 140 CATALTIC.

TO DOMAIN 361 CATALTIC.

TO DOMAIN 37 P55E8E35 CRC32;

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Best Local S
Matches 7
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EMBL; M18397; G153209; -.
PIR; A29912; A29912.
PIR; JH0573; JH0573;
HSSP; P07254; 1CTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIT_STRPL
P11220;
01-JUL-1989
01-DEC-1992
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 88087127.

ROBBINS P.W., ALBRIGHT C., BENFIELD B.;

J. BIOL. CHEM. 263:443-447(1988).

-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES

N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-I- INDUCTION: BY CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-45 FROM N.A., MEDLINE; 88087127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 92192480.
ROBBINS P.W., OVERBYE K.,
GENE 111:69-76(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREPTOMYCES PLICATUS. PROKARYOTA; FIRMICUTES;
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       379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CBD)
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dldweypnacglscdetsapnafssmmkamraefgqdylita-a---vtadgsdggk-id 433
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                                                                                                                                          h 10.5%;
Similarity 26.4%;
78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 11, CREATED)
(REL. 24, LAST SEQUENCE UP
(REL. 31, LAST ANNOTATION
3 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTINOMYCETALES;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                          Score 287; DB 2; L
Pred. No. 1.72e-35;
63; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                      Length 610
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                                                                                                                                            Indels .21;
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                                                                                                                                            Gaps
                                              114
                                                                                             378
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           -!- SIMILARITY: LOCAL, TO
-!- SIMILARITY: BELONGS T
EMBL; X07127; G2829; -.
EMBL; X00762; G2844; -.
EMBL; X01095; G2849; -.
PIR; S07915; O2915.
HSSP; P02877; 1HEV.
                                                                                                                                                              EUR. J. BIOCHEM. 199:483-488(1991).

-i- FUNCTION: THE ALFA SUBUNIT IS A POTENT EXOCHITINASE. ALONG WITH THE BETA SUBUNIT IT PLAYS A ROLE IN THE INTITAL INTERACTION OF THE BETA SUBUNIT IT PLAYS A ROLE IN THE GAMMA SUBUNIT (THE ACTIVAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR 1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDAT
KILLER TOXIN ALPHA AND BETA SUBUNITS PRECUR
(ENDOCHITINASE (EC 3.2.1.14)).
KLUYVEROMYCES LACTIS (YEAST).
PLASMID PGKL-1.
                                                                                                                                                                                                                                                                                                                                 MEDLINE; 87004569.
STARK M.J.R., BOYD A.;
EMBO J. 5:1995-2002(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 84297209.
STARK M.J.R., MILEHAM A.J., ROMANOS M.A.,
NUCLEIC ACIDS RES. 12:6011-6030(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTXA_
                                                                                                          TOXIN WITH SENSITIVE CELLS AND ALLOW THE GAMMA SUBUNIT ()
TOXIN) TO GAIN ENTRY INTO THE CELL.
-!- PTM: REZ IS POTENTIALLY SPLIT BY MEMBRANE-BOUND BASIC AM-
SPECIFIC PEPTIDASE TO YIELD THE ALPHA AND BETA SUBUNITS:
-!- SUBUNIT: THE KILLER TOXIN IS COMPOSED OF THREE SUBUNITS:
                                                                                                                                                                                                      BUTLER A.R., O'DONNEL R.W., MARTIN V.J., GOODAY G.W., EUR. J. BIOCHEM. 199:483-488(1991).
                                                                                                                                                                                                                                                                                  MEDLINE; 90259069.
BRADSHAW H.D. JR.;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 85037931. TOKUNAGA M., KAWAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOR F., FUKUHARA H.;
CURR. GENET. 9:147-155(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CBS 2359/152;
                                                                                                                                                                                                                             CHITINASE ACTIVITY OF ALPHA-SUBUNIT.
MEDLINE: 91301161.
                                                                                                                                                                                                                                                                     NATURE 345:299-299(1990).
                                                                                                                                                                                                                                                                                                         SIMILARITY TO CHITINASE
                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; FUNGI; ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P09805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546
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                                                                                                   BETA AND GAMMA.
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PS00026;
                                                                                                                                                                                                                                                                                                                                                                                                 KAWAMURA A., HISHINUMA F. S RES. 12:7581-7597(1984).
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CHITIN_BINDING
                                                                     S TO
                                                                                                                                                                                                                                                                                                          OF.
                                                                       OTHER CHITIN-BINDING FAMILY 18 OF GLYCOSY
                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                          ALPHA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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PRECURSOR
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                                                                         HYDROLASES
                                                                                                                                       BASIC AMINO ACID-
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                                                                                                                                                                                                                  STARK M.J.R.;
                                                                                                             ALPHA,
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                                                                                                                   Query Match
Best Local S
Matches 1
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Best Local S
Matches 6
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P30922;
01-UUL-1993 (REL. 26, CREATED)
01-UUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CARTILAGE GLYCOPROTEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGMENT).
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
PLASMID;
CHATIN DE
SIGNAL
PROPEP
CHAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
CARBOH
                                                                                                                                                                                                                                                                 GLYCOPROTEIN.
NON_TER
SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE: 88106603.

REJMAN J.J., HURLEY W.L.;

REJMAN J.J., HURLEY W.L.;

BIOCHEM. BIOPHYS. RES. COMMUN. 150:329-334(1988).

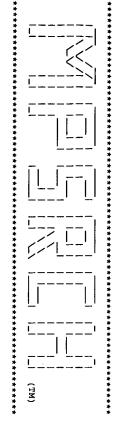
-I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE CAPACITY OF THE PROPRIED OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                     PIR;
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                                              N
                                                                                                                                                                                                                                                                                                                                                                         NONLACTATING PERIOD.
SUBCELLULAR LOCATION: EXTRACELLULAR.
SIMILARITY: BELONGS TO FAMILY 18 OF
27682; A27682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPOND TO AND COPE WITH CHANGES IN THI PTM: GLYCOSYLATED.
TISSUE SPECIFICITY: MANMARY SECRETIONS
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QQWLQK-GTPASKLILGMPTYGRSFTLASSS
klixyytswsqyregdgsxfpdaidpflxthviys 36
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Similarity 28.4%;
60; Conservative
                                                                                                                   Similarity 48.6%;
17; Conservative
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AA;
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11117
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4264 MW;
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Pred. No. 1.
58; Mismatc
                                                                                                           Score 172; l
Pred. No. 8.:
11; Mismatcl
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BETA SUBUNIT (PROBABLE).
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2 KLVCYFTNWAQYRQGEARFLPKDLDPSLCTHLIYA 36

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Search completed: Fri Jun 27 17:00:43 1997 Job time : 63 secs.



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fr1 Jun 27 17:08:30 1997; MasPar time 9.60 Seconds 423.400 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-663-618A-15 (1-373) from US08663618A.pep 2717 1 AKLYCYFTNWAQYRQGEARF......YPLIQTLRQELSLPYLSSGT 373

Scoring table:

PAM 150 Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 34.957; Variance 153.180; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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115 116 117 118	14889768486	Result No.
271 219 139 139 136 101	1328 1303 1303 1303 1303 1303 597 597 581 576 576 576 576	Score
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Factor-	Human factor VIII.	Human antihaemophilic	Human Factor VIII.	Human EGF receptor su	Bacillus stearothermo	Human BMP-6.		Human Bone Morphogene		ce1	Sequence encoded by t	rogen fi:	Sequence encoded by t	Protein encdoed by Mu	MuTu putative oncogen	YKL-40 internal pepti	0	Novel type III RTK en	Pre-pro-VGR1.	Glucoamylase encoded	Sequence of glucoamyl	Murine soluble epoxid		Murine BMP-9.
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ALIGNMENTS

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140 pg.rgsparorwtrvilleeligarkneag.tmrprillsaavsgopnvvgkayearilg 199 	klkernrglktllsiggwnfgtvrfttmlstfsnrerfvssviallrthgfdgldlffly	20 klycyftnwafsrpgpasilprdldpflcthlyfafasmsnnqivpkdpqdekilypefn 79	Query Match 48.9%; Score 1328; DB 14; Length 537; Best Local Similarity 51.2%; Pred. No. 9.77e-114; Matches 187; Conservative 74; Mismatches 97; Indels 7; Gaps	BOGP in high quantities. Sequence 537 AA;	Q90442 encodes R73991 bovine oviduct specific glycoprotein (BOGP). The cDNA can be used for the commercial recombinant prodn. of	recombinant protein production in high quantities. Claim 4; Pages 7-9; 22pp; Japanese.	New DNA encoding an oviduct-specific glycoprotein - useful for	WPI; 95-190179/25.	(KINO-) KINOSEI PEPTIDE KENKYUSHO KK.	15-AUG-1994; 21422/. 19-AUG-1993; JP-227881.	25-APR-1995.		/label= mat peptide 13)/	sig_pept	tide	Key Location/Qualifiers	Bos taurus.	BOATHE CAIGGE SPECIFIC GIACOPIOCETU: TECOMMINANT PROGUETION;	oviduct specific glycoprotein.	10-JAN-1996 (first entry)		LT 1 R73991 standard; Protein; 537 AA.

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J07107979-A.
25-APR-1995.
15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO KK
WPI; 95-190179/25.
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New DNA encoding an oviduct-specific glycoprotein - useful frecombinant protein production in high quantities.

Claim 4; Pages 16-18; 22pp; Japanese.

Q90444 encodes R73993 hamster oviduct specific glycoprotein The cDNA can be used for the commercial recombinant prodn. of HOGP in high quantities.

Sequence 668 AA;
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Matches 18
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/label= mai
J07107979-
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/label=
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RESULT 4
ID PRI342 standard; protein; 32
AC PRI342;
DT 19-OCT-1990 (first entry)
DE Polypeptide involved in prot
KW Immune response; cell growth
PN J63032898-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-1995.
15-AUG-1994; 214227.
19-AUG-1993; JP-227881.
(KINO-) KINOSEI PEPTIDE KENKYUSHO WPI; 95-190179/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 95-190179/25.

N-PSDB; 090443.

New DNA encoding an oviduct-specific glycoprotein - useful recombinant protein production in high quantities.

Claim 4; Pages 11-14; 22pp; Japanese.

090443 encodes R73992 murine oviduct specific glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-1996 (first entry)
Murine oviduct specific gl
Murine oviduct specific gl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAGFSCNQGRYPLIQT
                                                                                                                                                                                                                                         LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRIQDQ
                                                                                                                                                                                                                                                                                                                                                              QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                PGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               klkernrelktllsiggwnfgtsrftamlstlanrekfidsvisflrihgfdgldlffly
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19..718
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Similarity 49.9%;
182; Conservative
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               in protective growth.
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glycoprotein;
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Pred. No. 2.57e-111;
76; Mismatches 100;
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Best Local
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16-JUL-1986; 167518.
16-JUL-1986; JP-167518.
(DAIN) Dainippon Pharm K
WPI; 88-068419/10.
New plant protein having endo-chitinase activity - used in antifungal compans. and to develop transformed plants which are less susceptible to fungal infection.

Claim 3; Page 19-20; 43pp; English.

Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN tobacco plants with a probe derived from PRO840 (a partial Cluster-A cDNA clone) resulted in the isolated of 11 positively hybridising clones. Analysis revealed that all were identical and corresp. to Cluster-A cDNA. The nt sequence of clone cA-3 is given in Q82973/ R70025. This clone lacks 7 codons of the 5' part of the ORE. The cDNA clone was completed by performing a PCR reaction on clone cA-3 with primer T7 (082794) and primer P1 (Q82975). A partial AA sequence of the protein isolated from TMV-infected tobacco leaves
                                                                                                                                                                                                                                                                                                                                                                      Peptide
/label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R70025
R70025;
                                                                                                                                                                             Apotheker-de Groot M,
Melchers LS, Ponstein
WPI; 95-083454/12.
                                                                                                                                                                                                                17-AUG-1993; 202425.
17-AUG-1993; EP-202425.
(MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                                                                      Misc_difference 182..195
/note= "netarmin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; P81342.
New polypeptide and DNA encoding mechanisms such as immune respons
                                                                                                                                                                  N-PSDB; Q82973
                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco chitinase encoded by tol Tobacco; chitinase; antifungal;
                                                                                                                                                                                                                                                                                        /note= "Determined by protein sequencing"
Misc_difference 216..241
/note= "Determined by protein sequencing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                         JF, Cornelissen E
Sela-buurlage MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 881; DB 1;
Pred. No. 1.13e-70;
60; Mismatches 41
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New plant protein having endo-chitinase activity - used in antifungal compsns. and to develop transformed plants which are I antifungal compsns. and to develop transformed plants which are I less susceptible to fungal infection.

SC Claim 3; Page 25-28; 43pp; English.

Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN C tobacco plants with a probe derived from PROB40 (a partial Cluster-A CDNA clone) resulted in the isolated of 11 positively hybridising C clones. Analysis revealed that all were identical and corresp. to C cluster-A cDNA. The sequence of cDNA clone cA-3 is given in 082973/C R70025. A genomic library of N. tabacum was screened using the C cluster-A cDNA insert of clone cA-3 as a probe (see 082977, 082978).

The complete nt. sequence of Cluster-A cDNA including the deduced primary structure of the Cluster-A protein the 5 and 3 UTR regions C of the gene are shown in 082976/R70029. Comaprison of the cDNA
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deduced fr
Sequence
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R70029
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Melchers LS, Ponstein
WPI; 95-083454/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco cluster-A protein encode Tobacco; chitinase; antifungal;
                                                                                                                                                                                                    N-PSDB; Q82976
                                                                                                                                                                                                                                                                                  17-AUG-1993;
17-AUG-1993;
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Misc_difference 28..29
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107; Conser
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Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trichoderma harzianum pl endochitinase.
Trichoderma harzianum pl; endochitinase;
chitin containing fungi; herbivorous insc
Trichoderma harzianum.
                                                                                                                                                                                                                                                                    Example 8; Page 45; 62pp; English. 078144 encodes R63441 the Trichoderma harzianum Pl endochitinase, which can be used to inhibit chitin containing fungi and chitin containing herbivorous insects, especially from the genera below Fusarium, Gliocladium, Rhizoctonia, Trichoderma, Uncinula, Ustilage, Erysiphe, Botrytis, Saccharomyces, Sclerotium and Alternaria.
                                                                                                                                                                                                                                                                                                                                                                                                                              Trichoderma harzianum Pl endo:chitinase and cluseful in biological control of chitin-contg.
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L4-APR-1993; US-045269
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                                                                   QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL 116
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424 AA;
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larity 36.0%;
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3.42e-42;
tches 95;
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.07e-43;
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g. fungi and insec
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07-DEC-1993;
07-DEC-1992;
                                                                                                                                                                                                                                                                                                                         The sequence coding for wheat germin, a protein induced during germination of wheat, is a preferred example of DNA coding for a protein able to degrade oxalic acid. Such DNA can be coupled to sequence of interest, e.g. one coding for enzymes which confer resistance to pathogens (esp. endochitinases). Plant calli which have been successfully transformed by the sequences are selected by their ability to grow on oxalic acid-contg. medium. R56861 is a known sequence of a mature endochitinase; the sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= endochitinase WO9413790-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oxalic acid degradation; oxalate oxidase; filamentous fungus endochitinase; precurso pathogen resistance; plant cell selection
                                                                                                                                                                                                                                                                                                                                                                                                                                  cell selection, esp. gene coup
conferring pathogen resistance
pisclosure and Claim 8; Page 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 94-217870/
N-PSDB; Q68353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of gene encoding oxalic acid
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(ERAP ) SOC NAT ELF AQUITAINE.
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                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sdlgqvldyvnlmaydyagswssysghdanlfanpsnpnssp-yntdqaikdyikggvpa
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                                                                                                                                                   -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-1g 194
                                                                                                                                                                                         LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skivlgmpiygraf--estgg--igqtysgigs-gsw--engiwdy-kvlpkagatvqyd 336
||::|||| |||:| |:: :| :||: | |: | : ||| |
gcysydpstkelisfdtpamistkvswlkgkglggsmfw
                          LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                          lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak 305
                                                                                QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                            GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEV 176
                                                                                                                                                                                                                                              101;
                                                                                                                                                                                                                                                                                                    389
                                                                                                                                                                                                                                                                                                               disclosed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR-014721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    album.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                                                                                                                                                                                                             Score
Pred.
65; M
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d. No. 1.01e-41;
Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             degrading of to gene-en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                     French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme -
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Best Local S
Matches 10
JLT 10
R33068 standard; Prot
R33068;
30-JUN-1993 (first e
Aphanocladium album m
                                                                                                                                                                                                                                                                                                                                                                                                                mRNA by screening with anti-chitinase antiserum. Three probes were designed based on the CH3C sequence, corresponding to the start, middle and downstream regions of the coding sequence. The probes were used to isolate the full-length coding sequence of A.album endochitinase from an A.album cDNA library in p7219R. A 1.6kb fragment was identified in several positive clones. The sequence of the fragment contained an ORF encoding a 423 amino acid protein. The mature endochitinase can be used to control pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q37711, Q37712.

Recombinant DNA encoding fungal endo:chitinase - u protecting plants against fungi, insects, etc. Claim 1; Fig 1; 75pp; French.

Clone CH3C was isolated from a cDNA bank prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R33072
R33072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blaiseau P, Lego
WPI; 93-078700/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1992; 402414.
06-SEP-1991; FR-011072.
(SNFI ) ELF SANOFI.
(ERAP ) SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aphanocladium album.
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                                                                                                              340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      llamentous fungus; pathogen
                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                       h as fungi, bacc
mance 423 AA;
                                                                                     gcysydpstkelisfdtpamistkvswlkgkglggsmfw
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VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                    kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv
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                                                                                                                                                                                                                                                      lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp
                                                                                                                                                                                       QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                                                                                                                                         GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG
                                                                                                                                       LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                                                                                    lgmpiygrsfq-qt--eg-igkpyngigs-gsw--engiwdykalpk-agatvkcddtak
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- "pro-sequence"

in 35..423
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e 23..3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                         n 21.28;
Similarity 36.28;
101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Legoux R,
                                                                                                                                                                                                                                                                                                                                                                                                       bacteria, arthropods and nematodes on plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cocation/Qualifiers
                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423
  endochitinase
                                                                                                                                                                                                                                                                                                                                        Score 576; DB 6;
Pred. No. 1.01e-41;
65; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance
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                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                               378
                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                        -QTYVDAGYEVDKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.9%;
Best Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           filamentous fungus; pathogen resistance.
Aphanocladium album.
EP-531218-A.
10-MAR-1993: 402414.
06-SEP-1991; FR-011072.
(SNFI ) ELF SANOFI.
(EEAR ) SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                    22-AUG-1996.
13-FEB-1995; US-386727.
13-FEB-1995; US-386727.
(UYJO ) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Key
                    Chitin biosynthetic enzymes end I, exo I and exo I periplasmic chito:dextrinase(s), periplasmic beta-aryl beta-N-acetyl:gluco:amidase(s), respectively Example 4, Page 79-82; 101pp; English periplasmic chitodextrinase (W02156), periplasmic Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02158) can be used
                                                                                                                                                                                                                                Yu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 11
W02159 standard;
W02159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA encoding fungal endo:chitinase - useful for protecting plants against fung1, insects, etc. Claim 22; Page 60-61; 75pp; French.

This mature protein from the filamentous fungus Aphanocladium album has endochitinase activity and is used to control pathog such as fung1, bacteria, arthropods and nematodes on plants. Recombinant DNA comprising the endochitinase coding sequence specifically intended for transforming Nicotiana tabacum, Hell annus and Brassica napus to pathogen resistance. Sequence 389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplasmic chitodextrinase;
Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio furnissii.
WO9625424-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaiseau P, Legoux WPI; 93-078700/10.
                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; Q37704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
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                                                                                                                                                                                                      96-393335/39.
DB; T36390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPYIF-RD-NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-1g 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
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                                                                                                                                                                                                                                                                            Keyhani N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; periplasmic Beta-N-acetylglucosaminidase;
chitin; oligosaccharide; catabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 569; DB 6
Pred. No. 4.58e-
66; Mismatches
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No. 4.58e-41
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(GlcNAc)n where n
                                                                                                                                                                                                                                                                               Roseman
                                                                                                                                               exo II - are
beta-GlcNAcidase(s)
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encoded
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Disclosure; Fig. 1A-1C; 20pp; English.

Serratia marcescens QMB1466 genomic DNA was partially digested, ligated into vector pLARR1, packaged into lambda phage particles, and used to transfect Escherichia coll DH1 (ATCC 33849) cells.

Plating on chitin medium was used to screen for chitinase activity. Clone C12 (ATCC 67152) was isolated. Its sequence is given in 276290, and the deduced protein sequence in R64823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1986; US-888033.
09-JUL-1990; US-550253.
(DNAP ) DNA PLANT TECHNOLOGY
Jones JDG, Suslow T;
WPI; 95-035648/05.
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d. No. 3.52e-31;
Mismatches 104;
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Mismatches 126;
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Best Local
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01-MAR-1994, 593691.
26-MAR-1984, US-993691.
26-MAR-1984, US-993691.
18-JUL-1986, US-888033.
09-JUL-1990, US-550253.
14-AUG-1992, US-930970.
(DNAP ) DNA PLANT TECHNOLOGY CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibition of chitinous fungal plant pathogens - by transforming plant with DNA encoding chitinase activity

Disclosure; Fig.1; 13pp; English.

Plasmid pCHIT1251 containing the chitinase-A gene (chiA), fused directly to a nos promoter, may be used to transform, via Agrobacterium sp., a crop plant. The resulting transgenic plants expressing the chitinase-A protein fragment are protected against fungi, nematodes, insects and disease agents. The protein is preferably expressed by the plant only at the site of pathogen attack, e.g. only in the root cells. The plants express the chitinase in a biologically active form.

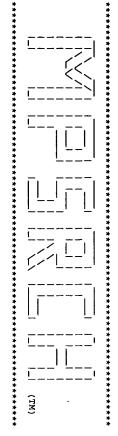
Sequence 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-1994 (first entry)
Bacterial chithase-A fragment from pCHIT1251.
Chitinase-A; enzyme; transgenic plant; biological control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R48981
R48981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 94-074348/09.
N-PSDB; Q57966.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones JDG,
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                                                                                                                                                                                                                                                                                                   alnar---pgsrhrlhhgerrecaagggvkpgkivvgtamygrgwtgvngyqnnipftgt
                                                                                                                                                                                                                                                                 AFAGMTNHQLSTTEWNDE-T-LYQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATAN
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alnar---pgsrhrlhhgegrecaagggvkpgkivvgtamygrgwtgvngyqnnipftgt
                                                                                        GSGTPGPFTKEGGMLAYYEVCS-WKGATKQ-RIQD-QKVPYIFR-DN-QWVGFDDVESFK
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                                                       EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KVTGHNS
                                                                                                                                                                                         hravkgtw--engivdyrqiasqfmsgewqytydataeapyvfkpstgdlitsddarsvq
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                                                                                                                                                              NRQTFVNSAIRFLRKYSF-DGLDLDWEYPGSQGS-PAV----DKERFTTLVQDLANAFQQ 147
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larity 27.6%;
Conservative
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84; M
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8.14e-23;
hes 125;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Matches 5
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Heliothis armigera nuclear polyhedrosis virus; Heliothis armigera nuclear polyhedrosis virus.
W09303144-A.
18-FEB-1993.
05-AUG-1992; AU0413.
05-AUG-1991; AU-007576.
Bassler
Yu C;
WPI; 96-
N-PSDB;
Chitin b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 51pp; English.
The sequence is that encoded by the Heliothis armigera (Ha) nuclear polyhedrosis virus (NPV) immediate early-1 (IE-1) gene (partial sequence).
Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-AUG-1991; AU-007576.
(CSIR ) COMMONWEALTH SCI &
Christian PD, Dall DJ, Gord
WPI; 93-076501/09.
N-PSDB: 015000
                                                                                                                                                                                                                                                                                Vibrio furnissii.
WO9625424-Al.
                                                                                                                                                                                                                                                                                                                                                                        Periplasmic chitodextrinase.
Periplasmic chitodextrinase;
Beta-N-acetylglucosamidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R32547;
17-JUN-1993 (first entry)
HanPV IE-1 gene protein (p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insect virus with reduced capacity for controlling proliferation of in
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                                                                                                                                                        13-FEB-1996; U02332.
13-FEB-1995; US-386727.
(UYJO) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                    catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W02156 standard;
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                                96-393335/39.
DB; T36387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNSPLYKRQEESGAAASLNVDAAVQQWL-QKGTPASKLILGMPTYGRSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVT-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRQTFVNSAI-R-F-L-RKYSFDGLDLDWEYPGSQGS-PAV-DKER----FTTLVQDLAN 143
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   biosynthetic
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Similarity 34.1%;
58; Conservative
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                                                                                                                           Chitlaru
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Pred. No. 9.44e-14
43; Mismatches 5
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chitin; oligosaccharide; catabolic;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:gluco:amidase(s), respectively Claim 2; Page 68-71; 101pp; English.
Periplasmic chitodextrinase (W02156), periplasmic Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02157) and aryl Beta-N-acetylglucosaminidase (W02158) can be used to produce chitin oligosaccharides with the structure (GlcNac)n where n is 2 or 'higher, by contacting them with soluble chitin. The enzymes are encoded by the genes endI, exoI and exoII respectively. They are all genes involved in the catabolic pathway of chitin.
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llarity 33.3%;
Conservative
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Pred.
40; M
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No. 3.13e-09;
Mismatches 42;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jun 27 17:04:42 1997; MasPar time 17.76 Seconds 598.666 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score:

Sequence: >US-08-663-618A-15
(1-373) from US08663618A.pep
2717
1 AKLVCYFINWAQYRQGEARF.....YPLIQTLRQELSLPYLSSGT 373

Scoring table: PAM 150 Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unanc 16:unrev

Statistics: Mean 47.342; Variance 104.126; scale 0.455

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1488 1428 1428 1417 1417 1318 1318 1318 1318 1018 598 582 582 582 444 446 446 446 346 347	Score
54.8 52.6 52.2 52.2 52.2 52.2 52.2 52.2 52.2	% Query Match 1
383 383 381 381 539 554 423 423 423 423 655 655 655 655 655 655 655 655 655 65	Length I
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A49562 S61550 S61550 S61550 S577879 S5278797 146470 A46470 A46470 A46470 A46470 A46470 A46470 A46470 A46470 A46470 A46470 A46651 A46651 A46651 A46651 A46651 A46651 A46651 A46633	ID
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1.77e-36 1.45e-28 1.50e-24 2.73e-21 1.45e-10 7.97e-10 9.06e-05 9.06e-05 9.06e-05 9.06e-01 1.02e-01 1.92e-01 8.92e-01 1.95e+00 1.9	u	alpha-glucosidase (E		membrane			umuC protein - Esche	probable coproporphy	chitinase (EC 3.2.1.	s with	(EC 3	2		oviduct-specific gly	estradiol-stimulated	whey protein	inase (EC 3.2	tinase (EC 3.2.	protein - yeas	glycoprotein -	(EC 3.2.	membrane	(EC 3.2.
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ALIGNMENTS

Db	Qy Db	Quer Best Matc	SUMMARY	FEATURE 1-21 22-383	KEYWORDS	9	# # 0		#ti	#jo	#au	REFERENCE				#ac		#ti	#jo	#au	REFERENCE	ACCESSIONS	DATE	ALTERNAT	TITLE	ENTRY	RESULT
83 lknrnpn	23 klvcyyt : 2 KLVCYFT	y Match Local Simi hes 195;	¥	383	DS takes	##molecule_	oss-referen				rs	NCE	##residues	##molecule_type mRNA	ß	accession				rs				E_NAMES			ч
lknrnpnlktlisvggwnfgsqrfskiasntqsrrtfiksvppflrthgfdgldlawlyp 142	klvcyytswsgyregdgscfpdaldrflcthiiysfanisndhidtwewndvtlygmlnt 82 : : : : : ::	Query Match 54.8%; Score 1488; DB 13; Length 383; Best Local Similarity 53.3%; Pred. No. 1.46e-250; Matches 195; Conservative 83; Mismatches 79; Indels 9; Gaps 5;	#label MAT #length 383 #molecular-weight 42613 #checksum 2942	#domain signal sequence #status predicted #label SIG\ #product cartilage glycoprotein gp39 #status predicted	cartilage; extracellular protein; glycoprotein	##MODECULE_type protein ###ODIECULE_type protein	cross-references MUID:90328983	povine manumary protein expressed during the non-lactating period.	Human synovial cells secrete a 39 kDa protein similar to a	Biochem. J. (1990) 269:265-268	Nyirkos, P.; Golds, E.E.	\$10677	##COSTORO TOFOTOSOR CR. MATABOOL HAK		preliminary	A49562	chondrocytes and synovial cells, is a mammalian member of a chitinase protein family.	Human cartilage gp-39, a major secretory product of articular	J. Biol. Chem. (1993) 268:25803-25810	Hakala, B.E.; White, C.; Recklies, A.D.	A49562	03-May-1996 A49562; S10677; A33162	23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change	#formal name Como carions #common name man	cartilage glycoprotein gp39 precursor - numan	A49562 #type complete	

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ACCESSIONS
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                        VPY1FRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAGFSCNQG-RYPL1QT
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1 Similarity 52.2%;
191; Conservative
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heparin-binding glycoprotein 38K - pig
#formal_name Sus scrofa domestica #common_name domestic
07-May-1995 #sequence_revision 07-May-1995 #text_change
07-May-1995
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1-383 ##label
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383 #molecular-weight 42443 #checksum
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Pred. No. 4.41e-239;
81; Mismatches 85;
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##residues 1-35
          preliminary;
##molecule_type mRNA
##residues
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##cross-references EMBL:X93035;
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186; Conservative
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##cross-references EMBL:X93035
# #length 381 #molecular-weight 43001
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                                                                                                                                        Morrison, B.W.; Leder, P.
Oncogene (1994) 9:3417-3426
neu and ras initiate murine mammary
markers generally absent in c-myc
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BRP39 protein - mouse
#formal_name Mus musculus #common_name house
02-Jul-1996 #sequence_revision 02-Jul-1996 #t
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BRP39 protein - mouse
#formal_name Mus musculus #common_name house mouse
10_Apr-1996_#sequence_revision 19-Apr-1996 #text_change
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Pred. No. 5.60e-237;
84; Mismatches 86;
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NID:g1085065; CDS_PID:g1085066
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##residues 1-399 ##label CHA
##cross-references EMBL:M94584
##CIOATION #superfamily Streptomyces chitinase chi40
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l Similarity 50.7%;
186; Conservativo
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Similarity 47.7%;
175; Conservative
                                                                                                                                                                                                                                                Chang, N.C.A.; Liu, C.H.; Chang, A.C. submitted to the EMBL Data Library, June 1992 Molecular characterization of a secretory protein transiently expressed by activated murine perito
                                                                                                                                                                                                                                                                                                            $27879 #type complete
secretory protein rM-1 precursor - mouse
#formal_name Mus musculus #common_name house mouse
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
03-May-1996
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Pred. No. 5.60e-237;
84; Mismatches 86;
                                                                                     Score 1345; DB 5;
Pred. No. 3.17e-223;
87; Mismatches 102;
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#length 537 #checksum 1695
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                   KVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAGFSCNQGRYPLIQT
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Similarity 51.2%;
187; Conservative
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Biol. Reprod. (1994) 50:927-934
Purification and molecular cloning
glycoprotein.
S57197
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Pred. No. 5.55e-220;
74; Mismatches 97;
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                           #accession
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                                                                                                                                                                                                                                                                                                                                                              LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRIQDQ
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Similarity 50.1%;
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estrogen dependent oviduct protein precursor - sheep
#formal_name Ovis orientalis aries, Ovis ammon aries
#common_name domestic sheep
16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
16-Aug-1996
                       Krishnan, A.; Nair, P.N.; Jones, D.
J. Biol. Chem. (1994) 269:20971-20976
Isolation, cloning, and characterization of new chitinase
stored in active form in chitin-lined venom reservoir.
A53918
                                                                                                           A5391
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erences EMBL:U16719; NID:g885600; CDS
#length 539 #molecular-weight 59535
                                                                                                                                    #formal_name Chelonus sp.
28-Jul-1995 #sequence_revision
                                                                                                                                                                           A53918 #type complete chitinase (EC 3.2.1.14) precursor
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Endocrinology (1995) 136:2485-2496
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             preliminary
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Pred. No. 4.49e-218;
77; Mismatches 98;
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#title Transmission-blocking antibodies recognize m
chithase in brugian lymphatic filariasis
#cross-references MUID:92179220
                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                      ##status preliminary; not compared
##molecule_type nucleic acid; protein
##residues 1-504 ##label_FUH
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1 Similarity 42.88;
158; Conservetion
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l Similarity 42.5%;
158; Conservative
                                                                                                                                                                sequence extracted from NCBI backbone glycosidase; hydrolase #length 504 #molecular-weight 55971 #che
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#length 483 #molecular-weight 52013
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Pred. No. 1.28e-191;
98; Mismatches 99;
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Pred. No. 5.49e-1
94; Mismatches 1
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                                                                                                           Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 37.4%;
Similarity 40.4%;
155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence extracted from NCBI backbone glycosidase; hydrolase #length 554 #molecular-weight 62203 #checksum
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Insect Biochem. Mol. Biol. (1993) 23:691-701
Sequence of a cDNA and expression of the gene encoding
epidermal and gut chitinases of Manduca sexta.
Sees MVID:93357793
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Chitinase (EC 3.2.1.14) - tobacco hornworm
#formal_name Manduca sexta #common_name tobacco hornworm
11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1015; DB 12;
Pred. No. 1.44e-160;
98; Mismatches 107;
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##cross-references EMBL:X78325
                 ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status
                 ##molecule_type mRNA
##residues_____1-378 ##label HEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEV-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPL-YKRQE-ESGAA-A-SLNVDAAVQQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEYP--GS-QG-S-PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 25.7%;
Similarity 40.1%;
                                                                                                                                                                                                                             s51591 #type complete
chitinase (EC 3.2.1.14)/lysozyme (EC 3.2.1.17) PZ precursor
pathogenesis-related - common tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
15-Jul-1995 #sequence_revision 08-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #superfamily fibronectin type III repeat homology
glycosidase; hydrolase
#length 699 #molecular-weight 73677 #checksum 6
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                                                                  Heitz, T.; Segond, S.; Kauffmann, S.; Geoffro, V.; Brunner, F.; Fritig, B.; Legrand, M. Mol. Gen. Genet. (1994) 245:246-254
Molecular characterization of a novel tobacco pathogenesis-related (PR) protein: a new pl. chirinase/lysozyme.
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Gene cloning of chitinase Al from Bacillus circulans
revealed its evolutionary relationship to Serratia
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chitinase [EG 3.2.1.14] precursor - Bacillus circulans
#formal_name Bacillus circulans
28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change
03-May-1996
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Pred. No. 2.65e-101;
73; Mismatches 85;
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##molecule_type protein

##residues 31-36;87-112;252-275;282-305;337-371 ##label HEW

ASSIFICATION #superfamily Streptomyces chitinase chi40
                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                             #description
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##residues
                 112
                                                                                                                                                                                      ##cross-references
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cession S51632
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                                             ch 21.4%;
l Similarity 36.0%;
102; Conservative
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Similarity 32.7%;
106; Conservative
                                                                                                                                                                                                                                                                                                 S47133 #type complete chitinase [EC 3.2.1.14) - fungus (Trichoderma harzianum) #formal_name Trichoderma harzianum 23-Nov-1994 #sequence_revision 03-Aug-1995 #text_change 10-May-1996 $47133 $47133 $47133 $47133 $Carsolio, C.; Gutierrez, A.; Jimenez, B.; van Montagu, Nerrera-Estrella, A.
                                                                                                     *superfamily Streptomyces chitinase chi40
glycosidase; hydrolase
#length 424 *molecular-weight 46298 #checksum
                                                                                                                                                                                                                                               endochitinase gene expressed during mycoparasitism S47133
                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1994 Characterization of ech-42, a Trichoderma harzianum
                                                                                                                                                      48/2; 81/2; 98/1
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#product chitinase/lysozyme PZ #status predicted
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Pred. No. 3.36e-82;
87; Mismatches 108;
                                                          Score 582; DB 5;
Pred. No. 5.18e-80;
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                                             Mismatches
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Best Local Similarity 36.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
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VPYIF-RD-NOWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                  QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
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                                                                                                                                  kvldyinlmaydyagswsnytghdaniyanpqnpnatp-yntddavqayinggvpankiv 287
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                                                       LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
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47/2;
                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label
#product chitinase 1 #status predicted #label MAN
#length 423 #molecular-weight 46072 #checksum 8802
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Gene (1992) 120:243-248
Primary Structure of chitinase-encoding gene (chi1) from
the filamentous fungus Aphanocladium album: Similarity to
bacterial chitinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Aphanocladium album 03-Feb-1994 #sequence_revision 0: 03-May-1996
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##molecule_type DNA
##residues 1-423 ##label GAR
SUMMARY #length 423 #molecular-weight 46056 #checksum 2000
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                                                             336 svækgyysynsætkellsfdtpdmintkvæylkslgiggsmfw 378 | | : ::|| ::|||:||| | ||||:| | 297 QDQKVPXIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW 337
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Curr. Genet. (1994) 27:83-89
Cloning and characterization of a chitinase (CHIT42) cDNA from the mycoparasitic fungus Trichoderma harzianum.
S51369
                                                                                                                                                                                                                                                                                                                                                                                            Gaps 13;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Jun 27 17:07:13 1997; MasPar time 12.20 Seconds 648.449 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-663-618A-15
(1-373) from US08663618A.pep
2717
1 AKLVCYFINWAQYRQGEARF......YPLIQTLRQELSLPYLSSGT 373

Scoring table: PAM 150 Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.971; Variance 85.460; scale 0.573

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221184 221174 221174 221174	Result No.
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1.03e-200 2.03e-200 2.13e-99 3.13e-99 8.30e-96 2.16e-92 7.16e-92 7.16e-92 7.16e-48 9.66e-48 9.66e-48 1.33e-58 9.66e-48 1.33e-58 9.66e-48 2.19e-35 1.86e-35 2.10e-92 2.16e-01 1.86e-35	Pred. No.

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EXTRACELLULAR SIGNAL-	BONE MORPHOGENETIC PR	HYPOTHETICAL 35.1 KD	ENDO-BETA-N-ACETYLGLU	VASCULAR ENDOTHELIAL	TY 3	H	KERATIN, TYPE II CYTO	SOLUBLE EPOXIDE HYDRO	SOLUBLE EPOXIDE HYDRO	PUTATIVE PROTEIN DISU	MOLYBDOPTERIN BIOSYNT	PUTATIVE PEPTIDASE IN	GTP CYCLOHYDROLASE II	HOMEOBOX PROTEIN MSX-	EXTRACELLULAR SERINE	L PR	KERATIN, TYPE II CYTO	KERATIN, TYPE II CYTO	KERATIN, TYPE II CYTO	LYSYL-TRNA SYNTHETASE	EXOTOXIN TYPE B PRECU	ALPHA-GLUCOSIDASE PRE
4.43e+00	4.43e+00	3.31e+00	3.31e+00	1.84e+00	2.47e+00	1.84e+00	1.84e+00	1.84e+00	1.36e+00	1.84e+00	2.47e+00	1.84e+00	2.47e+00	1.36e+00	7.44e-01	5.48e-01	1.01e+00	1.01e+00	1.01e+00	7.44e-01	5.48e-01	2.94e-01

ALIGNMENTS

Ma Ma	STITE OO
Query Match Best Local Matches 1	GP39_HUMP GP39_HUMP GP362221 01-JUL-11 01-JUL-
tch al sim 195;	GP39_HUMAN GP39_HUMAN FP36222; FP30923; O1-UUL-1993 (REL. O1-UUL-1994 (REL. O1-OUN-1994 (REL. O1-OUN-1996 (REL. CARTILAGE GLYCOPH HOMO SAPIENS (HUM EUKARYOTA; METAACE HUMAN PRIMATE [1] J. BIOL. CHEM. 26 SEQUENCE OF 22-45 MEDLINE; 94064658 MEDLINE; 94064658 SEQUENCE OF 22-45 MEDLINE; 94084 SEQUENCE OF 22-45 SEQUENCE OF 23-45 SEQUENCE OF 33-55 GIVCOPROTEIN; SIG GLYCOPROTEIN; SIG GLYCOPROTEIN; SIG GLYCOPROTEIN; SIG CARBOHYD CARBOHYD CARDON SEQUENCE 383 AA SEQUENCE 383 AA
Ë	GP39_HUMAN STANDARD; PRT; 383 AA. GP39_HUMAN STANDARD; PRT; 383 AA. P36222; P30923; Ol-JUL-1993 (REL. 25, CREATED) Ol-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) Ol-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) Ol-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) CARTILAGE ELYCOPROTEIN-39 PRECURSOR (GP-39) (39) HOMO SAPIENS (HUMAN). EUKHRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRA EUTHERIA; PRIMATES. [1] ISSUE-CARTILAGE; MEDLINE; 94064658. HAKALA B.E., MHITE C., RECKLIES A.D.; J. BIOL. CHEM. 268:25803-25810(1993). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BIOCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BIOCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BICCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BICCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BICCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; BICCHEM. J. 269:265-268(1990). SEQUENCE OF 22-45. MEDLINE; 90326983. NYIRKOS P. GOLDS E.E.; PRESPOND TO AND COPE WITH CHANCES IN THEIR E. -!- TISSUE SPECIFICITY: PRESENT IN ARTICULAR CH. CELLS AS WELL AS IN LIVER. UNDETECTABLE IN PANCREAS, MONONUCLEAR CELLS, OR FIBROBLASTS -!- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSY. EMBL; M80927; G348912; PIR; S10677; S10677. PIR; A33162; A33162. GLYCOPROTEIN; SIGNAL. SIGNAL 20 SARBOHYD 60 CARBOHYD 60 CARBOHYD 60 CARBOHYD 60 CARBOHYD 60 CARGOHYD 60 CARCOL 383 AA; 42613 MW; DOA5280F CRC32;
54.8%; arity 53.3%; Conservative	STANDARD; ;; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
** **	CREATED) LAST SEQUENCE LAST SEQUENCE LAST ANNOTATION TO PARTIAL SEQUENCE TO PARTIAL SE
Score 1 Pred. N 83; Mi	PRT; 38 SEQUENCE UPD. ANNOTATION UP RECURSOR (GP RECURSOR (GP) RECURSOR
1488; DB 4; No. 0.00e+00; Mismatches 79	(REL. 26, CREATED) (REL. 27, LAST SEQUENCE UPDATE) (REL. 34, LAST SEQUENCE UPDATE) (REL. 34, LAST SEQUENCE UPDATE) YCOPROTEIN -39 PRECURSOR (GP-39) IMATES MAY AND PARTIAL SEQUENCE. LAGE; LAGE; MAY ELS HITTE C., RECKLIES A.D.; M. 268:25803-25810(1993). 22-45. 28983. GOLUS E.E.; 269:265-268(1990). YEAS LOS THE HAMPORTANT ROLE IN THEIR TO AND COPE WITH CHANGES IN THEIR PECIFICITY: PRESENT IN ARTICULAR WELL AS IN LIVER. UNDETECTABLE IN YOUNONUCLEAR CELLS, OR FIBROBLAS COSYLATED. YOUNGLE GLYCO YOUNGLE GLY
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Best Local S
Matches 15
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P29030;
01-DEC-1992
01-DEC-1992
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SEQUENCE
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PIR; A38221; A38221.
PROSITE; PS01095; CHITINASE_18.
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MEDLINE; 92179220.
FUHRMAN J.A., LANE V
                                                                                                                                                               SIGNAL
                                                                                                                                                                        REPEAT;
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 u
                                                                                                                                                                                                                                                                                                                    KMAN J.A., LANE W.S., SMITH R.F., PIESSENS W.F., PERLER F.B.;
C. NATL. ACAD. SCI. U.S.A. 89:1548-1552(1992).
FUNCTION: THE MEI ANTIGEN IS A MICROFILARIAL CHITINASE, WHICH
FUNCTION TO DEGRADE CHITIN-CONTAINING STRUCTURES IN THE MICRO-
FILARIA OR IN ITS MOSQUITO VECTOR DURING PARASITE DEVELOPMENT
TRANSMISSION.
                                                                                                                                                                                                                                    KNOWN TO BIND CALCIUM.

DEVELOPMENTAL STAGE: THE APPEARANCE OF THE MET ANTIGEN CORRESPOND WITH THE ONSET OF THE PARASITE'S ABILITY TO INFECT THE MOSQUITO. SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                       N-ACETYL-D-GLUCOSAMINE PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                                                HYDROLASES)
           ::: |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ikdala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRIQDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYFTNWAQYRQGEARFLPKDLDPSLCTHLIYAFAGMTNHQLSTT-EWNDE-T----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAGFSCNQG-RYPLIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              м73689;
                                             th 40.0%;
Similarity 42.8%;
158; Conservative
                                                                                                                                                                       GLYCOSIDASE; CHITIN DEGRAD. YCOPROTEIN; CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                            METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL. 24, CREATED)
(REL. 24, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
(SE PRECURSOR (EC 3.2.1.14) (MF1 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365
                                                                                                                                                                                                                  G156064; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                      22
504
400
450
448
148
                                                                                                                                                                                                                                                                                                                                                                                                     AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                           ACOELOMATES; NEMATODA; SECERNENTEA;
                                                                                          55971
                                                                                                                                                                                                                                                                                                            HYDROLYSIS
                                                                                          ¥.
                                                                                                                                                                                                                                                                                                   POLYMERS
                                           Score 1086; DB 2;
Pred. No. 1.03e-218;
94; Mismatches 102;
                                                                                    ENDOCHITINASE.
CATALYTIC.
SER/THR-RICH (LINKER).
SER/THA-RICH (LINKER).
3 X 14 AA APPROXIMATE TANDEM REPEATS.
3 Y 14 AA APPROXIMATE TANDEM REPEATS.
PROTON DONOR (BY SIMILARITY).
; 4DA7E5EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                   DEGRADATION;
                                                                                                                                                                                                                                                                                                 OF THE BETA-1,4
S OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTIGEN).
                                                                                                                                                                                   SIGNAL;
                                                                  Length
                                                                                                                                                                                                                                                                                                            LINKAGES
                                                                                                                                                                                   ANTIGEN;
                                             15;
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OXT
                                           Gaps
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MAY

AND

57

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23

arivcyfsnwavyrpgvgrygiedipvekcthiiysfigvtegnsev1lidpeldvdkng |::||||:|| | | ; |: |: |||:||:|: : : | | : |

Gaps

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  Query Match
Best Local S
Matches 15
                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                         CHAIN
DOMAIN
ACT_SITE
CARBOHYD
CARBOHYD
                                                                                                                           HYDROLASE;
SIGNAL
                                                                                                                                                 EMBL; S6
HSSP; P0
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; LEPIDOPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIT_MANSE
P36362;
                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                  KRAMER K.J., CORPUZ L., CHOI
INSECT BIOCHEM. MOL. BIOL. 2
-!- FUNCTION: DIGEST CHITIN
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 93357793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                  BUT RAPIDLY DISAPPEARS AND IS UNDETECTED ON DAYS 1-4 OF FIFTH INSTAR. IT REAPPEARS ON DAY 5 AND PEAKS ON DAY 7 AFTER WHICH A RAPID DECLINE IS SEEN. IN THE GUT IS DETECTED ON DAY 6 WITH LOWER LEVELS SEEN ON DAYS 0, 7 AND 8.

TISSUE SPECIFICITY: EPIDERMIS AND GUT.
SUBCELLULAR IOCATION: SECRETED.
                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                           N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

DEVELOPMENTAL STAGE: HIGH LEVELS SEEN IN THE EPIDERMIS ON DAY
                                                                                                                                                                                            HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hqegvgaymvkgdqwygydneetirikmkwlkekgyggafiwaldfddftgkscgkgpyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U02270; G400
S64757; -; I
P07254; ICTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIQTLRQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       llnaissel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDQKV-PYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMVWALDLDDFAGFSCNQGRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSW-KGATKQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPAS
   155;
            Similarity
                                                                                                                            GLYCOSIDASE;
1 19
                                         1
20
396
146
146
303
407
545
  Conservative
                                                                                                                                                            1CTN.
                                                                                                                                                                                G406049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                     NOT_ANNOTATED_CDS
                                                                                                                                      CHITINASE_18.
IDASE; CHITIN DEGRADATION;
                                          554
453
146
85
303
407
545
62203
            37.4%;
                                                                                                                                                                                                                                                                                                                    CHOI H.K., MUTHUKRISHNAN OL. 23:691-701(1993). ITIN IN THE EXOSKELETON DU
                                           WW.
 Score
Pred.
98; M
                                                             ENDOCHITINASE.
SER/THR-RICH.
PROTON DONOR (B
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                         POTENTIAL.; FA87F8AD
                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
re 1015; DB
1. No. 7.72e-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         554
                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA
                                                                                              (BY
 2;
107;
                                                                                                                                       SIGNAL;
                                                                                                                                                                                                                                                                                                                     DURING
                     Length
                                                                                                                                                                                                                                                                                                                                         S
 Indels
                                                                                                                                       GLYCOPROTEIN.
                     554;
 24;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 93366760.

WATANABE T., KOHORI K., MIYASHITA K., FUJII T., SAKAI H.,

UCHIDA M., TANAKA H.;

J. BIOL. CHEM. 268:18567-18572(1993).

-1- CAPALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES OF N-ACETYL-D-GLOCOSANIE POLYMERS OF CHITIN.

-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF G
                                                            ACT_SITE
MUTAGEN
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991 (REL.
01-FEB-1991 (REL.
01-FEB-1995 (REL.
                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WATANABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACILLUS CIRCULANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHITINASE A1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHI1_BACCI
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                    HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS
                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P20533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL.
                                                                                                                                                                                                                                                                                                             A38368; A38368.
P07254; 1CTN.
                                                                                                                                                                                                                                                                                                                                                                           HYDROLASES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEVDKIAQNIDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yhvpelcqeldaihvmsydlrgnwagfadvhsplykrphdqwayeklnvndglhlweekg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDWEYPGS--QGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frnftslrsshpsvkfmvavggwaegsskyshmvagkstrmsfirsvvsflkkydfdgld
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                                                                                                                                                                                                                                                                                       7254; 1CTN.
PS01095; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90368776.
T., SUZUKI K., OYANAGI W., OHNISHI
CHEM. 265:15659-15665(1990).
                                                                                                                                                                                                                                                                                                                                                      G142688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                   41
699
460
549
644
200
200
200
200
204
73677
                                                                                                                                                                                                                                                                    CHITINASE_18.
IDASE; CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17, CREATED)
17, LAST SEQUENCE UPDATE)
31, LAST ANNOTATION UPDATE)
URSOR (EC 3.2.1.14).
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOSPORE-FORMING
                                                                ĭ
                                                                           CATALYTIC.

FIBRONECTIN TYPE-III (R-1).

FIBRONECTIN TYPE-III (R-2).

FROTON DONOR (PROBABLE).

D-N: DECREASE IN ACTIVITY.

D->E: NO CHANGE IN ACTIVITY.

E->D,Q: LOSS OF ACTIVITY.
Score 698; DB 2; I
Pred. No. 2.43e-127;
                                                                                                                                                                                                                           CHITINASE A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                            ->D,Q: LOS
5A1777CC
                                                                                                                                                                                                                                                                  DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×;
                                                                                                                                                                                                                                                                  SIGNAL;
                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cocci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H .;
                                                                                                                                                                                                                                                                                                                                                                                            OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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01-FEB-1996
01-FEB-1996
CHITINASE 1
                                                                                                                                                                                                                                                                                                  CHAIN
ACT_SITE
SEQUENCE
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P32470;
                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ETHM 483;
MEDLINE; 93013040.
BLAISEAU P.-L., LAFAY J.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APHANOCIADIUM ALBUM.
EUKARYOTA; FUNGI; DEUTEROMYCOTINA (IMPERFECT FUNGI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLAISEAU P.-L., KUNZ C., GRISON R., CURR. GENET. 21:61-66(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X64104; G429026;
PIR; JQ1975; JQ1975.
HSSP; P07254; ICTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 35-57.
MEDLINE; 92136437.
                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
      229
                                                122
                                                                                      174
                                                                                                                                                    115 lkkqnrnmkvmlsiggwtwst-nfpaaassaatrktfaqsavgfmkdwgfdgididweyp 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R. GENET. 21:01 TYPE HYDROLIUS.
R. ACTIVITY: HYDROLIUS.
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHILL
N-MRCELLULAR LOCATION: SECRETED.
THRCELLULAR TOTOMCS TO CHITINASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hldagvpaaklvlgvpfygrgwd-gcaqagn-ggygtctggssvgtweagsfdfydlean 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ntelakiaaivdwinimtydfngawqkisahnaplnydpaasaagvpdantfnvaagagg
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                                            GSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG-QTYVDAGYEVDKIA
                                                                         -adatqaqnmvlllqavrseldsyaaqy-akg-hhfllsiaapagpdnynklkfa-e-lg 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120:243-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W--K-GATKQRIQDQKVPYIFRD-NQW-VGFDDVESFKTKVSYLKQKGLGGAMVWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYEVDKIAQNLDEVNLMAYDEHGSWEKVTGHNSPL-YKRQE-ESGAA-A-SLNVDAAVQQ
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                                                                                                                              LKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLDWEYP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEV-CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEYP--GS-QG-S-PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDLD
                                                                                                                                                                                                                101;
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                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  PS01095;
                                                                                                                                                                                                                                                                                                                        SO1095; CHITINASE_18.
GLYCOSIDASE; CHITIN DEGRADATION;
1 22 POTENTIAL.
23 34 POTENTIAL.
35 423 CHITINASE 1.
171 171 PROTON DONOR (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REL. 27, (REL. 33, REL. 33, PRECURSOR
                                                                                                                                                                                                                                                                                                    423 AA;
                                                                                                                                                                                                                21.2%;
larity 36.2%;
Conservative
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. 33, LAST SEQUENCE UPI
. 33, LAST ANNOTATION U
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                                                                                                                                                                                                                Score
Pred.
65; M
                                                                                                                                                                                                                                                                                                  CHITINASE 1.
PROTON DONOR (BY
88456E6E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                    576; DB 2;
No. 3.13e-99;
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S OF CHITIN.
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                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FAMILY
                                                                                                                                                                                                                                                        Length 423
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                                                                                                                                                                                                             Gaps
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PROPEP
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CURR. GENET. 27:83-89(1994).
-!- FUNCTION: MORPHOGENETIC ROLE DURING APICAL GROWAND DIFFERENTIATION (CELL WALL MORPHOGENESIS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (REL.
01-FEB-1996 (REL.
01-FEB-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND MEDLINE; 95269313.
GARCIA I., LORA J.M., LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRICHODERMA HARZIANUM.
EUKARYOTA; FUNGI; DEUTEROMYCOTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHI4_TRIHA P48827;
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HYDROLASE; GL
                                     336
                                                                        237
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-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
KD ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENT.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-ACETYL-D-GLUCOSAMINE POLYMERS SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: SPECIFICALLY
                      svakgyysynsatkelisfdtpdmintkvaylkslglggsmfw
                                                                                                                                                                QEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYSFDGLDL 116
                                                                                                                                                                                                                                                                                                              QDQKVPYIFRD--NQWVGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                            DKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK 300
                                                                      SKLILGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRI
                                                                                                                                                                                                                    DWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAGQTYVDAGYEV
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101; Conser
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171
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423 /
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                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                           Score 561; DB 2;
Pred. No. 8.30e-96;
71; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
899DA50A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 KD ENDOCHITINASE
PROTON DONOR (BY SIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE BETA-1,4
CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APICAL GROWTH, CELL DIVISION HOGENESIS). ANTIFUNGAL
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                                                                                                                                                                                                                                                                                                                                                                                                Length 423;
                                   378
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THE SULPT PROCESS OF SUCCESS OF S
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                                                                                                                                                     RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUI
01-OCT-1996 (REL. 34, LAST ANNO:
ENDOCHITINASE 1 PRECURSOR (EC 3
(CE-ANTIGEN) (CF-AG).
               P07254;
01-APR-1988
01-FEB-1995
01-FEB-1995
CHITINASE A
CHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
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CARBOHYD
CONFLICT
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EMBL; U51271; G1256769;
EMBL; U33265; G1255728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C735;
MEDLINE; 96144270.
PISHKO E.J., KIRKLAND T
GENE 167:173-177(1995).
SERRATIA MARCESCENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SILVEIRA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCCIDIOIDES IMMITIS EUKARYOTA; FUNGI; DEI
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                                                                                                                                   CHIA_SERMA
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                                                                                                                                                                                                          VPYIF-RDNOW-VGFDDVESFKTKVSYLKQKGLGGAMVW
                                                                                                                                                                                                                                                                                                                                                              QNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLI
                                                                                                                                                                                                                                                                                                                                                                                  kyldfwnlmaydfsgswdkvsghmsnvfpsttkp-estpfssdkavkdyikagvpankiv
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                                                                                                                                                                                                                                            asysydknkrylisydtvkiagkkaeyitkngmgggm-w
                                                                                                                                                                                                                                                                                                       lgmplygraf--ast-dg-igtsfngvgg-gsw--engvwdykdmpg-ggaqvteledia
                                                                                                                                                                                                                                                                                 LGMPTYGRSFTLASSSDTRVGAPATGSGTPGPFTKEGGMLAYYEVCSWKGATKQRIQDQK
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95; Conser
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427 /
                                   (REL. 07,
(REL. 31,
(REL. 31,
PRECURSOR
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387
15
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                                                                                                                               STANDARD;
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34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
THE TROOP (EC 3.2.1.14) (COMPLEMENT-FIXATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEUTEROMYCOTINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%;
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47629
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427
387
47
                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(EC 3.2.1.14).
                                                                                              CREATED)
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ENDOCHITINASE 1.
POTENTIAL.
RWLSLRCLFCELGRFMFTLSTVTAVTVVTDDIQ ---
RWLSLRCLFCELGRFMFTLSTVTAVTVVTDDIQ ---
SMSNKNYYPVPEAPEGGFRSVVYFVNW (IN REF
K -> N (IN REF. 2).
WW; 6CB9AF73 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 546; | Pred. No. 2.: 71; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLE
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                                                                                                                                 563
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.16e-92;
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BETA-1,4 LINKAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                          337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 -> 1
REF.
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Best Local S
Matches 9
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EMBL; X03557; G46831; -.
PIR; A25090; A25090.
HSSP; P07254; ICTN.
PROSITE; PS01095; CHITINASE_18.
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SEQUENCE FROM N.A.
KOO J.C., LIM C.O., C
                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-i- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE; 95219379.
PERRAKIS A., TEWS I., DAUTER Z., OPPENHEIM A.B., CHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
JONES J.D.G., GRADY K.L.,
EMBO J. 5:467-473(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE 2:1169-1180(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \begin{array}{lll} \textbf{PROKARYOTA}; & \textbf{GRACILICUTES}; & \textbf{SCOTOBACTERIA}; & \textbf{FACULTATIVELY} & \textbf{ANAEROBIC} & \textbf{RODS}; \\ \textbf{ENTEROBACTERIACEAE}. \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VORGIAS C.E.;
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                                                                                                                                                                                            349
321
                                                                               464
                                                                                                           206
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              akgkyvldkqlgglfsweidadn 545
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                                                                                                                                                                                                                     atg-pvkgtwkngivdyrgiaggfmsgewqytydataeapyvfkpstgdlitfddarsvq
                                                                                                           PLYKRQEESGAAASLNVDAAVQQWLQKGTPASKLILGMPTYGRSFTLASSSDTRVGAPAT
                                                                                                                                   alnapawkpdtayt-tvng-vnallaqgvkpgkvvvgtamygrgwtgvngyqnnipftgt
                                                                                                                                                                               TKVSYLKQKGLGGAMVWALDLDD
                                                    GSGTPGPFTKEGGMLAYYEVCS-WKGATKQ-RIQD-QKVPYIFR-DN-QWVGFDDVESFK
                                                                                                                                                                EAQTSGKERLLLSAAVPAGQTYVD-AGYEVDKIAQNLDFVNLMAYDFHGSWE-KVTGHNS
                                                                                                                                                                                                                                                                                                                                 Similarity 28.8%;
93; Conservative
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563
315
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391
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226
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467
473
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                                                                                                                                                                                                                                                                                                                                                                                           WW;
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V -> I (IN REF. 2).
P -> A (IN REF. 1 AND 2).
P -> A (IN REF. 1 AND 2).
PAWKPDTAXTTYNGVUNALLAQ -> RPGSRHRLHHGERRQC AAGQ (IN REF. 1 AND 2).
V -> I (IN REF. 2).
ATGP -> HRA (IN REF. 2).
K -> E (IN REF. 2).
G -> S (IN REF. 2).
MW; 7764DB57 CRC32;
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                                                                                                                                                                                                                                                                                                                                   Score 437; DB 2;
Pred. No. 7.14e-68;
84; Mismatches 123
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CATALYTIC.
PROTON DONOR (PROBABLE).
343
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TA -> GP (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGRADATION;
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                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 9

ID CHIT_NPVAC
AC P41684;
DT 01-NOV-1995
DT 01-NOV-1995
DE POBABLE ENI
OS AUTGCRAPHA (
OC VIRIDAE; DS-
RN [1]
RP SEQUENCE FR
RC STRAIN-C6;
RX MEDLINE; 94.
RA AYRES M.D.,
RA AYRES M.D.,
RA AYRES M.D.,
RA OF CONTROLAR
CC -1- CATALYT
CC -1- CATALYT
CC -1- CATALYT
CC -1- STRAIN-CS;
RY PROSITE; PS
DR 
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Best Local S
Matches 9
                                                                                                  CHIA_ALTSO
P32823;
01-OCT-1993
01-OCT-1993
01-FEB-1995
CHITINASE A
VIBRONACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYRES M.D., HOWARD S.C., KUZIO J., LOPEZ-FERBER M., POSSEE R.D.;
VIROLOGY 202:586-605(1994).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
HYDROLASES).
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PROBABLE ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
AUTOGRAPHA CALLFORNICA NUCLEAR POLYHEDROSIS VIRUS
VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE;
                                         ALTEROMONAS PROKARYOTA;
                                                                                     CHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94303173.
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95; Conser
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173
444
548
551
                                         SP. (STRAIN 0-7)
GRACILICUTES; SC
                                                                                                     (REL. 27, CREATED)
(REL. 27, LAST SEQUENCE UI
(REL. 31, LAST ANNOTATION
PRECURSOR (EC 3.2.1.14) (
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larity 29.2%;
Conservative
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173
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CHITIN DEGRADATION;
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                                         SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 395; DB 2; Le
Pred. No. 1.33e-58;
80; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE ENDOCHITINASE.
PROTON DONOR (BY SIMILARITY).
POTENTIAL.
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                                                                                                                                                                                                                PRT;
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                                                                                                     ON UPDATE)
(CHI-A).
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EUBACULOVIRINAE
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                                           ANAEROBIC
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RESULT ACCOUNTS OF THE PROPERTY OF THE PROPERT
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Best Local S
Matches 5
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MEDLINE; 93106952.
TSUJIBO H., ORIKOSHI H., TANNO H.
IMADA C., OKAMI Y., INAMORI Y.;
PACTERIOL. 175:176-181(1993).
                                                                                                                                                                                                                                                                                                             CHIB_SERMA
P11797;
01-OCT-1989
01-OCT-1989
01-FEB-1995
                                                   HARPSTER M.H., DUNSMUIR P.;
NUCLEIC ACIDS RES. 17:3395-5395(1989).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4
N-ACETYL-D-GLICCOSAMINE POLYMERS OF CHITIN.
-I- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
ACT_SITE
SEQUENCE
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 PIR;
                    EMBL;
                                                                                                                                                                                                                       SERRATIA MARCESCENS.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAN.
                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 990 / QMB1466;
MEDLINE; 89345110.
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MEDLINE; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSUJIBO H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROLASES).
L; D13762; G216207; -.
19; P07254; 1CTN.
DSITE; PS01095; CHITINASE 18.
STYCOSIDASE; CHITIN DEGRADATION;
HYDROLASES)
3L; X15208; G4
8; S04856; S04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAG IN-ACETYL-D-GLUCOSAMLER POLYMERS OF CHITIN.

ENZYME REGULATION: STIMULATED BY MG2+; INHIBITED BY N-BROMOSUCCINIMIDE AND 2-HYDROXY-5-NITROBENZYL BROMII SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18
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57; Conser
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(REL. 12,
(REL. 31,
PRECURSOR
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larity 35.0%;
Conservative
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                  G47228;
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313
87346
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AND TEMPERATURE
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INAMORI Y.;
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                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(EC 3.2.1.14).
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                                                                                                                                                                                                                                        SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
44; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHITINASE A.
PROTON DONOR (BY SIMILARITY).
838F6EE8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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No. 9.
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).66e-48;
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                                                      (FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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                                                      GLYCOSYL
                                                                                        얽
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                                                                                                                                                                                                                                        RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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                                                                              Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                    MEDLINE; 93294525.

FUJII T., MIYASHITA K.;

J. GEN. MICROBIOL. 139:677-686(1993).

-i- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4
                                                                                                                                                                                                                                                                                                                                                                                                         CHIT_STRLI
P36909;
01-JUN-1994
01-JUN-1994
01-FEB-1995
CHITINASE C
                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                 HYDROLASE;
SIGNAL
CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P07254; 1CTN.
PROSITE; PS01095; CHITINASE_18.
HYDROLASE; GLYCOSIDASE; CHITIN DEGRADATION;
SIGNAL 1 41
CHAIN 42 499 CHITINASE B.
ACT_SITE 144 144 PROTON DONOR (F
                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                        - -
                                                                                                                                                                                                                                                                                                                                                                                        STREPTOMYCES
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                              EMBL; D12647; G391910; HSSP; P07254; 1CTN.
                                                                                                                                                                                                                                                           + +
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                   PROSITE;
                                                          311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
  107
                    369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                      N-ACETYL-D-GLUCOSAMINE INDUCTION: BY CHITIN. SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ltalkahnps1rimfs19gwyysnd1gvshanyvnavktpaartkfagscvr1mkdygfd 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAGYE-VDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDLDWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERL--LLSAAVPAGQTYV
RKYS-FDGLDLDWEYPGSQG-S--PAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAA
          rwadvfdgidldweypnacglscdetsapnafssmmkamraefgqdylita-a---vtad
| |||:|||||| : | | : :::: | | |: :: ::|
                                        WNDETLYQEFNGLKKMN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gvdidweyp--qaa-evd-g-fiaalqeirtllnqqtiadgrqalpyqltiagaggaffl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNGLKKMNPKLKTLLAIGGW---N-FG-TO-KFTDMVATANNRQTFVNSAIRFLRKYSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 54; Conser
                                                                             h 11.1%;
Similarity 28.2%;
86; Conservative
                                                                                                                                                                                      PS00018; EF_HAND.
PS00561; CBD_BACTERIAL.
PS01095; CHITINASE_18.
E; GLYCOSIDASE; CHITIN DEGRADATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
42
144
499 /
                                                                                                                    1
31
35
148
240
240
382
619 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 29,
(REL. 29,
(REL. 31,
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                              FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                         LIVIDANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                            N.A.
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                                                                                                                                                                                                                                                          CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
499 C
144 P
55464 MW;
                                                                                                                              30
619
140
230
619
382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.4%;
                                                                                                                     65200 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPI
LAST ANNOTATION (
(EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                                                                                                                                             ACTINOMYCETALES;
                                      -PKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFL
                                                                                                                                                                                                                                                           >
⊢
                                                                                                                                                                                                                                                                                       CHITINASE CLASS II (FAMILY
                                                                                                                                                                                                                                                          FIBRONECTIN TYPE III-LIKE DOMAIN BACTERIAL-TYPE CELLULOSE-BINDING
                                                                                                                                      POTENTIAL.
CHITINASE C.
CELLULOSE-BINDING.
FIBRONECTIN TYPE-III.
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
47; 1
                                                                            Score 301; DB 2;
Pred. No. 2.19e-38;
65; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                   PROTON DONOR (BY SIMILARITY).
23E3E1EC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHITINASE B.
PROTON DONOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9A585FFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337; DB 2;
No. 5.03e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          619
                                                                                                                                                                                                                                                                                                                                                                                                                   UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                             STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                              129;
                                                                                                                                                                                       CHITIN-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                              Indels
                                                                                                                                                                                                                                                                                                                    LINKAGES
                                                                                                619;
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                                                                              25;
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                                                                                                                                                                                                                                                                                                                     ဝ္ဗ
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                       GLYCOSYL
                                                                            Gaps
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 162
                  424
                                      106
                                                                              18;
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RESULT TO SEE THE PROPERTY OF SEE THE 
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                                                                                                                                                  Matches
                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 92192480.
ROBBINS P.W., OVERBYE K
GENE 111:69-76(1992).
[2]
                                                                                                                                                                                                                                            DOMAIN
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROBBINS P.W., ALBRIGHT C., BENFIELD B.;
J. BIOL. CHEM. 263:443-447(1988).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF THE BETA-1,4 LINKAGES
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-I- INDUCTION: BY CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M82804; G153216; -. EMBL; M18397; G153209; -. PIR; A29912; A29912. PIR; JH0573; JH0573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ++
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHITINASE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIT_STRPL
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROKARYOTA;
  379
                                                                                               320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425
                                                56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROLASES).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TE; PS00018; EF_HAND.
TE; PS00561; CBD_BACTERIAL.
TE; PS01095; CHITINASE_18.
TE; PS01095; CHITINASE_63.
CHITINASE_63.
CHITINASE_63.
CHITINASE_63.
THE 35 140 CELLULOSE-BINDING.
THE 148 229 FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYEVCSWKGATKQRIQDQKVPYIFRDNQWVGFDDVESFKTKVSYLKQKGLGGAMYWALDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gsdggk-idaa-dygeaskyidwynvmtydffgawak-ngptaphspltaydgipqqgfn
: | :|: : | |:|:|| | : |: ::|
dldweypnacglscdetsapnafssmmkamraefggdylita-a---vtadgsdggk-id 433
                                              YQEFNGLKKMNPKLKTLLAIGGWNFGTQKFTDMVATANNRQTFVNSAIRFLRKYS-FDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDFAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P07254; 1CTN
                                                                                                                                             h 10.6%;
Similarity 26.4%;
78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88087127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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(REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRECURSOR
                                                                                                                                                                                                                                                 AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11,
24,
31,
                                                                                                                                                                                                                                              63974 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
R (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALBRIGHT
                                                                                                                                                                                                                                       CHITINASE 63.
CELLULOSE-BINDING.
FIBROMECTIN TYPE-III.
CATALYTIC.
PROTON DONOR (BY SIMILARITY).
F -> I (IN REF. 2).
MW; 2F5EBE35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHITINASE CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE III-LIKE DOMAIN. BACTERIAL-TYPE CELLULOSE-BINDING
                                                                                                                                               Score 287; DB 2;
Pred. No. 1.86e-35;
63; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ر</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဝှု
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II (FAMILY
                                                                                                                                               134;
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                        -!- SIMILARITY: LOCAL, TO
-!- SIMILARITY: BELONGS T
EMBL; X07127; GS829; -.
EMBL; X00762; G2844; -.
EMBL; X01095, G2849; -.
PIR; S07915, S07915.
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOR F., ESOR F., GENET.
                                                                                                                                                                                 MEDLINE; 91301161.

BUTLER A.R., O'DONNEL R.W., MARTIN V.J., GOODAY G.W., STARK M.J.R.;
EUR. J. BIOCHEM. 199:483-488(1991).

-I. FUNCTION: THE ALPHA SUBUNIT IS A POTENT EXOCHITINASE. ALONG WITH
THE BETA SUBUNIT IT PLAYS A ROLE IN THE INTERACTION OF THI
TOXIN WITH SENSITIVE CELLS AND ALLOW THE GAMMA SUBUNIT (THE ACTIV.)
TOXIN) TO GAIN ENTRY INTO THE CELL.

-I. PUM: RP2 IS POTENTIALLY SPLIT BY MEMBRANE-BOUND BASIC AMINO ACID-
-I. PUM: RP2 IS POTENTIALLY SPLIT BY MEMBRANE SUBUNITS.
-I. SUBUNIT: THE KILLER TOXIN IS COMPOSED OF THREE SUBUNITS: ALPHA,
BETA AND GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDAT
KILLER TOXIN ALPHA AND BETA SUBUNITS PRECUR
(ENDOCHITINASE (EC 3.2.1.14)).
KLUYVEROMYCES LACTIS (YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY TO CHITINASE OF MEDLINE; 90259069.
BRADSHAW H.D. JR.;
NATURE 345:299-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 87004569.
STARK M.J.R., BOYD A.;
EMBO J. 5:1995-2002(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 84297209.
STARK M.J.R., MILEHAM
NUCLEIC ACIDS RES. 12:
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SOR F., FUKUHARA H.;
CURR. GENET. 9:147-155(1985)
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S RES. 12:7581-7597(1984).
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Best Local 9
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P30922;
01-UL-1993 (REL. 26, CREATED)
01-UL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CARTILAGE GLYCOPROTEIN-39 (GP-39) (39 KD WHEY PROTEIN) (FRAGMENT).
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.

SEQUENCE.

SEQUENCE.

REJMAN J.J., HURLEY W.L.;

BIOCHEM. BIOPHYS. RES. COMMUN. 150:329-334(1988).

-I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE CAPACITY OF RESPOND TO AND COPE WITH CHANGES IN THEIR ENVIRONMENT.

-I- PTM: GLYCOSYLATED.

-I- TISSUE SPECIFICITY: MAMMARY SECRETIONS COLLECTED DURING NONLACTATING PERIOD.

-I- SUBCELLULAR LOCATION: EXTRACELLULAR.

-I- SIMILARITY: BELLONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01095; CHITINASE_18.
PLASMID; TOXIN; GLYCOPROTEIN; SIGNAL; HYDROLASE; GLYCOSIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                425 ddsafsksaflkvtssk-k-ipsfggwdfstspstytifrnavktdqnrntfannlinfm 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 ywylkn-fpisdiqntvdymvymtydihgiwe--ygkans-yi---nchtprk-eiedai 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 QTYVDAGYEVDKIAQNLDFVNLMAYDFHGSWEKVTGHNSPLYKRQEESGAAASLNVDAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 nkynldgidldweypgapdipdipaddsssgsnyltflkllkgkmps-gktl-siaipss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 9.7%;
Local Similarity 28.4%;
nes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                          N
klixyytswsqyregdgsxfpdaidpflxthviys 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQWLQK-GTPASKLILGMPTYGRSFTLASSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKYSFDGLDLDWEYPGSQGSPAVDKERFTTLVQDLANAFQQEAQTSGKERLLLSAAVPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETLYQEFNGLKKMNPKLKTLLAIGGWNFGT-Q-KFT---DMVATANNRQTFVNSAIRFL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEGRADATION.
                                                                                                          h 6.3%;
Similarity 48.6%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 99
1082 108
1117 11:
1146 AA;
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4264 MW;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
                                                                                                      Score 172; DB 4; L
Pred. No. 8.53e-13;
11; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 263; DB 5; Le
Pred. No. 1.67e-30;
58; Mismatches 74;
                                                                                                                                                                                                                                             F3935740 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA SUBUNIT (PROBABLE).
BETA SUBUNIT (PROBABLE).
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1146;
                                                                                                                                                                      Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 19;
                                                                                                          Indels
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